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February 4, 2006, 15:40:16; Search time 2893 Seconds (without alignments) 18733.937 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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of donors with active replication of known viruses. Inactive proviruses can be detected and inactivated, allowing identification and elimination of potential human pathogens derived from swine in a manner not possible in the outbred human organ donor population and is important to the development of human xenotransplantation
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The invention relates to purified nucleic acid molecule that can specifically hybridise with the sequence of swine retroviruses. The nucleic acid is useful in methods for determining the copy number or nucleic acid is useful in methods for: determining the copy number or care a proxime retrovirus from a human; screening a cell, tissue or human being for the presence or expression of a porcine retrovirus or retroviral sequence; assessing the potential risk associated with the transplantation of a graft from a donor miniature swine or swine retrovirus or retroviral sequence genome includes a mutation that modulates its expression; providing a swine free of an endogenous retrovirus or retrovirus squence; evaluating a treatment for the ability to activate a retrovirus; localising the origin of a porcine retrovirus; and inhibiting expression of an endogenous porcine retrovirus; and detecting a recombinant virus or other pathogens, e.g. protozoa or fungi. The present sequence represents miniature swine retrovirus; considering the origin of a porcine retrovirus;
                                                                              New purified nucleic acid molecules that specifically hybridize with swine retroviral sequences, useful for detecting the presence of porcine retrovirus, e.g., for assessing the potential risk associated with the
                                                                                                                                                                                                                          Claim 6; SEQ ID NO 3; 82pp; English
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100.0%; Score 8132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8132; Conservative 0; Mismatches
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                                                                                                     Location/Qualifiers
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                                                                    endogenous retrovirus
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13-DEC-1996; 96US-00766528.
14-SEP-2000; 2000US-00661858.
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This cDNA sequence represents a porcine retrovirus from miniature swine containing the putative coding regions for viral GAG, POL and ENV containing the putative coding regions for viral GAG, POL and ENV controls. This sequence and POR fragments generated from it (see AAT74812 T74882) can be used to screen organs for the presence of porcine retroviruses prior to xenotransplantation. Transplantation can increase the likelihood of retroviral activation if intext and infectious proviruses are present. The porcine retroviral sequence can be used to generate probes to determine the level (e.g. copy number) of intext (i.e. potentially replicating) porcine provirus sequences in a strain of contentially replicating porcine provirus sequences in a strain of contential lesions or viral recombinants and also to determine the histological localisation of activated retrovirus. Using Polymerase Chain thration and susceptibility testing can be performed. Ultimately animal donors without intext porcine retroviral sequences or a lower copy number of viral elements could be selected. (Updated on 27-AUG-2003 to correct
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100.0%; Pred. No. 0;
ive 0; Mismatches
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New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of transmitting infection to graft recipient.
                                                                                                                                                                                                                                                                                                                                                                     8041 GGGCCGCAGTCCTCTACCCCTGCGTGTGTACGACTGTGGGCCCCAGCGCGCTTGGAATA
                                                                                                           CCACGAAGCGCGGGCTCTCGAAGTTTTAAATTGACTGGTTTGTGATATTTGAAATTGACT
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TCCATGAACAAGCTTAGAGAAAGGTTGGAGAAAGCGTCGAAGGGAAAAGGAAACTACTCAA
                                                                                                                        7441 TTAATTGCCTTCATTAGAGAACGAATAAGTGCAGTCCAGATCATGGTACTTAGACAACAG
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                                                                                  ACAGGACCCTTAATAGTCCTCCTCTTACTCACAGTTGGGCCATGTATTATTAACAAG
                                                                                                                                                                        7501 TACCAAAGCCCGTCTAGCAGGGAAGCTGGCCGCTAGCTCTACCAGTTCTAAGATTAGAAC
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pig breeding; chromosome mapping; protection; ds.
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This invention describes novel replication-competent molecular clones of porcine endogenous retrovirus (PERV) isolated from a porcine BAC (C Charterial artificial arthromosome) library which are replication competent after transfer into permissive cells. The invention also discloses (a) env and gag polypeptides encoded by the molecular clones of the invention of sequences of the integration site of a replication competent molecular clone in the porcine genome; (c) oligonucleotides for detecting sequences of the integrated PERV; (d) a method for detecting experience of infectious PERV particles in a sample; (e) a vaccine for immunization against replication competent PERV, comprising an env protein and (f) a method for isolating competent PERV, comprising an env protein and (f) a method for isolating competent PERV, comprising an env protein and (f) a method for isolating competent PERV, comprising an env protein and (f) a method for isolating competent pervices of the invention are charmed activity. The clones are from native PERV and make possible comparisons of proviral sequences of different origins at the molecular, comparisons of proviral sequences of different origins at the molecular, correctural and callular levels, and mapping of proviral sequences at the clones of the invention are useful for comparisons against replication-competent perv or protection against replication-competent form the products of the invention are useful for protection against replication-competent, full-length, proviral constant a pervice of the invention are produced by the clones of the invention are useful for protection against replication-competent, full-length, proviral constants a pervice of the invention are perpendents a PERV. The products of the invention are perpendents a PERV. The products of the invention are perpendents a pervice of the invention are perpendents a PERV. The product of the invention are perpendents a PERV. The product of the invention are perpendents and perpendents and perpendents and perpendents 1037 349 409 469 619 229 289 917 797 857 858 écréricircadacceraaceacrececeacrerearcaccacacerecraceacearc 679 GATTŤTAACTCGAČTGGCCŤŤTČÁGŤTGČTGGTTGGČCĞĞGAAACCČĞĞĞAĞTAČČČ TAACACCCGAGAACCGACTTGGAGGTAAAAGGATCCTCTTTTTAACGTGT--ATGCATG 230 TACCGGCCCCGCCTCTCTGTTTCTGTTTTTCAGTGCTGCCCCTTTCGCTTTGCA reresecrescerererererastrerereritreserarisceeritreserriteser GCTGTCCTCTCAGGCCGTAAGGGCTGGGGACTGTGATCAGCAGACGTGCTAGGAGGATC 918 ACAGGCTGCCACCCTGGGGGACGCCCCGGGAGGTGGGGAGGCCAGGGACGCCTGGTGGT 978 crecrrererescreasesacesacricierieriesasecesasecricecereces ----TICITITIGCIGGICITACATITIGGGGCTCGTCCGGGATCTGTCGCGGCCACCCC CTCCTACTGTCGGTCAGAGGACCGAATTCTGTTGCTGAAGCGAAAGCTTCCCCCTCCGCG GCGTGGTGTACGACTGTGGGCCCCCAGCGCGCTTGGAATAAAAATCCTTGCTGTTTGCA TCAAGACCGCTTCTCGTGAGTGATTAAGGGGAGTCGCCTTTTCCGAGCCTGGAGG----ACAGGCTGCTGCCCTGGGGGACGCCCCGGGAGGTGAGGAGGAGGCCAGGGACGCCTGGTGGT Gaps Sequence 8918 BP; 2435 A; 2174 C; 2253 G; 2056 T; 0 U; 0 Other; Indels 164; ; 548; DB ; Score 6931.2; ; Pred. No. 0; 0; Mismatches Query Match 85.2%; Best Local Similarity 91.4%; Matches 7574; Conservative 172 798 350 410 61 116 739 290

1097

590 ACAGACGGTGACGACCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAG 649

470 ACCGTCCGACTCTTTTGCCTGCTTGTGGAAGACGTGGACGGGTCACGTGTGTCTGGATCT

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This invention describes novel replication-competent molecular clones of porcine endogenous retrovirus (PERV) isolated from a porcine BAC (C (bacterial artificial athromosome) library which are replication competent after transfer into permissive cells. The invention also discloses (a) env and gag polypeptides encoded by the molecular clones of the invention of a replication competent molecular clone in the porcine genome; (c) oligonucleotides for detecting sequences of the integrated PERV; (d) a method for detecting appearance of infectious PERV (c) a method for detecting appearance of infectious PERV (c) a vaccine for immunization against replication competent PERV, comprising an env protein and (f) a method for isolating the molecular clones of the invention. The products of the invention are competent PERV, comprising an env protein and (f) a method for isolating the molecular clones of the invention. The products of the invention are comperisons of proviral sequences of different origins at the molecular, structural and cellular levels, and mapping of proviral sequences at comparisons of proviral sequences of different origins at the molecular, comparisons of proviral sequences of the invention are useful for protection against replication-competent PERV. The products of the invention are functional, replication-competent, full-length, proviral colones isolated directly from the pig genome, i.e. they are 'native' colones isolated directly from the pig genome, i.e. they are 'native' colones isolated directly from the pig genome, i.e. they are 'native' colones isolated the invention are perfected in the product of the invention are perfected in the product of the invention are perfected to the invention are perfected in the product of the invention are perfected in the product of the invention are perfected in the
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                                                                                                                                                                                                                                                                                 porcine; env; gag; infection; vaccine; virucide; immunization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8918 BP; 2428 A; 2174 C; 2254 G; 2061 T; 0 U; 1 Other;
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                                                   The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
         aB
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by introducing recombinant DNA comprising {\sf DNP} proteins of the agent into donor cells, such
                                                                                                                                                323;
                                                                                                           Sequence 7873 BP; 2200 A; 1913 C; 1962 G; 1798 T; 0 U; 0 Other;
                                                                                                                             4; Length 7873;
                                                                                                                                                352; Indels
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                                                                                                                             Score 6531.8; I pred. No. 0; 0; Mismatches 3
                                    16; Page 112-115; 144pp; English.
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                                                                                                                             Query Match 80.3%;
Best Local Similarity 91.4%;
Matches 7166; Conservative C
transplant recipients,
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This invention describes novel replication-competent molecular clones of porcine endogenous retrovirus (PERV) isolated from a porcine BAC (bacterial artificial chromosome) library which are replication competent after transfer into permissive cells. The invention also discloses (a) env and gag polypeptides encoded by the molecular clones of the invention; (b) porcine nucleic acids that represent the 5' and 3' flanking
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sequences of the integration site of a replication competent molecular clone in the porcine genome; (c) oligonucleotides for detecting clone in the porcine genome; (c) oligonucleotides for detecting spearance of infectious PERV competent a sample; (e) a waccine for immunization against replication competent PERV, comprising an env protein and (f) a method for isolating the molecular clones of the invention. The products of the invention are comparisons of proviral sequences of different origins at the molecular, structural and callular levels, and mapping of proviral sequences at chromosomal positions in specific breeds of pigs. Also different breeds configurately PERV-free animals. Also vaccines that contain the env configuration are functional, replication-competent, full-length, proviral clones isolated directly from the pig genome, i.e. they are 'native' prove solated directly from the pig genome, i.e. they are 'native' prover of the invention are functional, replication-competent, full-length, proviral clones isolated directly from the pig genome, i.e. they are 'native' prover of the invention are functional, replication-competent sexible in the constant of the invention are functional, replication-competent (i.e. they are 'native' prover of the invention are functional, replication-competent fasment described in the constant of the invention are functional, replicating from the pig genome, i.e. they are 'native' prover the pig genome are the pig genome, i.e. they are 'native' prover the pig genome are the pig genome, i.e. they are 'native' prover the pig genome are the pig genome, i.e. they are 'native' prover the pig genome are the pig genome ar

1023 115 531 591 651 711 291 351 843 411 903 471 547 909 999 231 723 783 171 9 CGTCCGACTCTTTTGCCTGCTTGTGGAAGACGCGGACGGGTCGCGTGTGTCTGGATCTGT CTCATAATTTGTCAGTTCAGGTTAAGAAGGGACCTTGGCAGACTTTCTGTGTCTCTGAAT TCAAGACCGCTTCTCGTGAGTGATTAAGGGGAGTCGCCTTTTCCGAGCCTGGAGG----TAACACCCGAGAACCGACTTGGAGGTAAAAGGATCCTCTTTTTAACGTGTATGCATGTA TGTCCTCTCAGGCCGTAAGGGCTGGGGGACTGTGATCAGCAGACGTGCTAGGAGGATCAC AGACGGTGACGACCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGG eceregretaceacreresececeaececeresearaaaarecrerregrafireea CCGGCCGCCTCTCTGTTCTGAGTGTCTGTTTTCAGTGCGCGCTTTCGGTTTGCAGC AGGCTGCTGCCCTGGGGGACGCCCCGGGAGGTGAGGAGAGACGCCAGGGACGCCTGGTGGTCT CCTACTGTCGGTCCAGAGTCCGAGTTCTGTTGTTGAAGCGAAAGCTTCCCCCTCCGCGGC CGTCCGACTCTTTTGCCTGCTTGTGGAAGACGTGGACGGGTCACGTGTGTCTGGATCTGT TGGTTTCTGTTTTTGTCTTTGTGTGTGTCCTTGTCTACAGTTTTAATATGGGAC GCGTGGTGTACGACTGTGGGCCCCCAGCGCTTGGAATAAAAATCCTCTTGCTGTTTGCA ----TICITITIGCIGGICITACAITIGGGGGCICGICCGGGAICIGICGCGGCCACCCC GATTGITCITITACTGGCCTTTCATTTGGTGCGTTGGCCGGGAAATCCTGCGACCCC Gaps Score 6319; DB 6; Length 8763; Pred. No. 0; 0; Mismatches 941; Indels 126; Query Match
Best Local Similarity 87.0%;
Matches 7159; Conservative 607 199 1024 1084 844 532 592 ч 232 412 472 964 652 488 61 172 292 784 352 904 116 g ઠે g δ 셤 ઠ 셤 셤 g g δ g ò 쉽 원 엄 8 Š 8 ò ઠે ઠે ઠે

1371 1863 1431 1923 1491 1983 1551 2043 1611 2103 1671 2163 1731 2223 1791 2283 AGGCTGAGTTACGTGATCTAGTGAAGGAGGCAGAGAAGTATATTACAAAAGGGAGACAG 1851 1503 1191 1683 1251 1743 1311 1803 101 1563 1131 1623 1443 101 831 TTATAGGACAGTCAGCCTTGGATATTAGAAAGAAGCTTCAGAGACTGGAAGGGTTACAGG 2224 TCATTGGGCAGTCGGCTCTGGATATCAGAAAAAACTTCAGAGACTGGAAGGGTTACAGG rctrcacaacceaegaegaegaaartrctertagaegctagaaaaartetrcegeg CCGACGGCGACCCACGCGGTTGCAAATGAGATTGACATGGGATTTCCCTTAACTCGCC TGGTGGCGGGTCTCCGGGGCGCCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAAG TGGTGGGTCTCCGGGGCGCCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAGG TGATGCAGGGACCGAATGAACCCCCTCTGTTTTTTTTGAGAGGCTCTTGGAAGCCTTCA GGCGGTACACCCCTTTTGATCCCACCTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCCT cretraagecaarcatritricagacregaccegecretearcearcagagecerara TCCTTACGTGGCAAGATTTTGGCAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATA AAAAAGTCAAGCCCTCTCCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGG AACCCCAATCTGTTCCCCCACCCCTTATCTGGCACAGGGTGCCGCGAGGGGACCCTTTG CCCCTCCTGGAGCTCCGGCGGTGGAGGGACCTGCTGCAGGGACTCGGAGCCGGAGGGGCG CCACCCCGGAGCGGACAGACGAGATCGCGACATTACCGCTGCGCACGTACGGCCCTCCCA CCACCCCGGAGCGGACAGACGAGATCGCGATATTACCGCTGCGCACCTATGGCCCTCCCA CACCGGGGGCCCAATTGCAGCCCCTCCAGTATTGGCCCTTTTCTTCTTCTGCAGATCTTATA ATTGGAAAACTAACCATCCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGG AGTCCCTTATGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACAC TCTTCACAACCGAGGAGGAGAGAATTCTATTAGAGGCTAGAAAAAATGTTCCTGGGG 1924 CCGACGGCGACCCACGCAGTGCAAAATGAGATTGACATGGGATTTCCCTTGACTTGACT GGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAGATTATCCTGG CTGTTAAAGCAGTTATTTTCAGACTGGACCCCGGCTCTCATCCCGATCAGGAGCCCTATA 1252 1984 2164 1792 1192 1744 1312 1804 1372 1864 1432 1492 1552 2044 1612 2104 1732 1504 1564 1204 1264 1324 1384 1012 1072 1132 1624 952 1444 712 772 832 892 В g 셤 g ઠે 셤 ò g ઠે 요 셤 셤 ₽ 요 ò g Š 셤 ઠે g ð ð ò ò 유 8 8 ò g ò 8 g 8 ď ઠ

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                                                                                                                                                          Replication-competent molecular clones of porcine endogenous retrovirus, useful as sources of env peptides for vaccination and for viral
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                                                                                                                                                                                                                                                                                                                                                                                                  932; Indels 155; Gaps
                             i) porcine; env; gag; infection; vaccine; virucide; immunization;
breeding; chromosome mapping; protection; ds.
                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 8840;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 8840 BP; 2307 A; 2227 C; 2315 G; 1991 T; 0 U; 0 Other;
                                                                                                                    (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST,
                                                                                                                                                                                                                                                                                                                                                                                   Score 6288.8; 1; Pred. No. 0; 0; Mismatches 9
                PERV clone PK15-PERV-B(Bac-192B9)
                                                                                                                                                                                      Claim 8; Fig 17; 52pp; German.
                                                  Porcine endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                                                                      77.3%;
86.8%;
                                                                                         09-MAR-2001; 2001DE-01011433
                                                                                                      09-MAR-2001; 2001DE-01011433
    (first entry)
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                                                                                                                                              WPI; 2002-699548/76.
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                                                               DE10111433-A1
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101 1541 1071 1131 1661 1191 1721 1251 1481 AACCCCAACCTGTTCCCCCCACCCCTTATCCAGCACAGGGTGCTGTGAGGGGACCCTCTG 1601 1781 ATTGGAAAACTAACCATCCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGG 1311 1421 1181 1241 1301 1361 1001 1061 1121 531 591 651 711 771 831 891 951 471 821 881 411 941 291 351 TGTCCTCTCAGGCCGTAAGGGCTGGGGACTGTGATCAGCAGGACGTGCTAGGAGGATCAC rercitcreacceralegacreaceacrererareaccerecregaceace AGGCTGCCACCCTGGGACGCCCTGGGAGGTGGGGAGGCCAGGGACGCCTGGTGGTCT CCTACTGTCGGTCAGAGGGACCGAATTCTGTTGCTGAAGCGAAAGCTTCCCCCTCCGCGAC ceracrerederedadeseceserrerereseseses ecreeceses TGGTTTCTGTTTTTGTCTTTGTCTTGTGTCCTTGTCTACAGTTTTAATATGGGAC 1062 regrircierriceferererireferirerecerecriererekentrinarararegeae AGACGGTGACCCCCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGG CTCATAATTTGTCAGTTCAGGTTAAGAAGGGACCTTGGCCAGACTTTCTGTGTCTCTGAAT GGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAGATTATCCTGG GGCCAACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAAATTATCCTGG CTGTTAAAGCAGTTATTTTCAGACTGGACCCGGCTCTCATCACCGATCAGGAGCCCTATA TCCTTACGTGGCAAGATTTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATA 952 AAAAAGTCAAGCCCTCTCCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGG <u> AAAAAGTCGAGCCCTCTCCTCGTATCTACCCCAAGATCGAGGAGCCGCCGACTTGGCCGG</u> AACCCCAATCTCTTCCCCCACCCCTTATCTGGCACAGGGTGCCGCGAGGGGACCCTTTG CCACCCGGAGCGGACAGACGAGATCGCGACATTACCGCTGCGCACGTACGGCCCTCCCA CACCGGGGGGCCAATTGCAGCCCCTCCAGTATTGGCCCTTTTCTTCTGCCAGATCTCTATA AGGCTGCTGCCCTGGGGGGCCCCGGGAGGTGAGGAGGCCAGGGACGCCTGGTGGTCT CGTCCGACTCTTTTGCCTTGTGGAAGACGTGGACGGGTCACGTGTGTCTGGATCTGT CCGGCCGGCGTCTCTGTTCTGAGTGTCTGTTTTTCAGTGGTGCGCGCCTTTCGGTTTTGCAGC

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*tag= 1
note= "Binding site for transcription factor BTS-1/GATA"
793. .7834
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'note= "Binding site for transcription factors AP-1/GATA,
--Myb and AP-1"
1928. .7953
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note= "Binding site for transcription factors GATA, ETS-
, c-Myb, AP-1, GATA, E47"
7841. 7851
*tag= n
note= "Binding site for transcription factor AP-1"
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/note= "Binding site for transcription factor AP-1/CREB"
8075..8090
/*tag= x
8127..8135
/*tag= z
/*note= "PolyA downstream element"
8161..8166
/*tag= aa
/*tag= h
/note= "U3 LTR domain"
7643. .7686
/*tag= 1
/note= "Binding site for transcription factors OCT-1, c-
yyb, LyP-1, E47 and ETS-1"
                                                                                                                     *tag= j
note= "Binding site for transcription factors AP-4 and
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note= "Binding site for transcription factors E47 and
TS-1"
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note= "Binding site for transcription factor AP-1/TR"
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$185. .7997
*tag= mBinding site for transcription factor GATA"
003. .8007
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note= "Binding site for transcription factor GATA"
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note= "Binding site for transcription factor AP-1"
885. .7914
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P-PSDB; AAW39271, AAW39273.
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97GB-00002668.
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985. .7997
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10-FEB-1997;
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                                                                                                                                          7866 CCCACCCCGAAACAIGCGCAAA---IGTGTAACTCTAAAACAATITAAATTAATTGGTCC 7922
                                                                                                                                                                   8484 CTATTTTAAAATGATTGGTCCACGGAGCGGGCTCTCGATATTTTAAAATGATTGGTCC 8543
                                                                                                                                                                                                        7923 ACGAAGCGCGCGCTCTCGAAGTTTTAAATTGACTGGT-------TTGTGATA 7967
                                                                                                                                                                                                                                                                                                                                        8028 GACTCCACACTCGGGGCCGCAGTCCTCTACCCCTGCGTGGTGTACGACTGTGGGCCCCAG 8087
             AAACTATTTGAGATAACAAGAAAAGGGAGTTTCTAACTGCTTGTTTAGCTTCTGTAAAAC 7805
                                                                                                          8424 CTATCTCAACTGCAATCTGTCACTCTGCCCAGGAGCCCACGCAGATGCGGACCTCCGGAG 8483
                                                                                                                                                                                                                            8364 ATTĊTGTAAAACTGACTGGCACCATAGAAGAATTGATTACACATTGACAGCCCTAGTGAC 8423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine retrovirus; PoEV; POL protein; ENV protein; GAG protein; virion core polypeptide; polymerase protein; envelope protein; vaccine; diagnosis; xenotransplantation; prophylactic; therapeutic; ds.
                                                                                                                                                                                                                                                                          7968 TTTTGAAATGATTTGTAAAGCGCGGGCTTTGTTGTGAACCCCATAAAAGCTGTCCC
                                                                                                                                                                                                                                                                                            Porcine retrovirus DNA encoding the LTR and GAG, POL and ENV proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGCTTGGAATAAAATCCTCTTGCTGTTTGCATCAAAA 8127
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product= "POL protein"
note= "polymerase peptide"
620. .7590
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/product= "ENV protein"
/note= "envelope protein"
7591. .8209
7638. .8106
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product= "GAG protein"
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*tag= c
note= "U5 LTR domain"
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*tag= a
note= "R LTR domain"
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*tag= y
note= "R LTR domain"
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(first entry)
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/*tag= l
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                 Polynucleotide encoding porcine retrovirus expression product - useful to develop products for use in vaccines, diagnosis and xeno-transplantation.
                                                                                This DNA sequence encodes the porcine retrovirus (PoEV) virion core polypeptide (GAG), polymerase (POL) and envelope (ENV) proteins and also includes the Long Terminal Repeat (LTR). These proteins can be used to develop viral vaccines, antisence of ancieic acids, ribozymes and other antiviral agents. They can also be used in xeno-transplantation technology and as diagnostic tools. (Updated on 27-AUG-2003 to correct OS
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Matches 7165; Conservative
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Porcine retrovirus, PoEV, POL protein; ENV protein; GAG protein, vaccine; diagnosis; xenotransplantation; prophylactic; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding porcine retrovirus expression product - useful to develop products for use in vaccines, diagnosis and xeno-transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA sequence encodes the porcine retrovirus (PoEV) virion core polypeptide (GAG), polymerase (POL) and envelope (ENV) proteins. These proteins can be used to develop viral vaccines, antisense nucleic acids, ribozymes and other antiviral agents. They can also be used in xenctransplantation technology and as diagnostic tools. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                          The present invention provides a method to prevent the transmission of infectious agents during xenotransplantation. This involves introducing to donor swine cells a recombinant DNA encoding a peptide fragment from the infectious agent, and then introducing these cells into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting or preventing infectious agent transmission in mammalian transplant recipients, by introducing recombinant DNA comprising DNA encoding extracellular proteins of the agent into donor cells, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGCTCTCGATATTTTAAAATGATTGGTTTGTGACGCACAGGCTTTGTTGTGAACCCCA
                                                                                                                                     TAAAAGCTGTCCCGACTCCACACTCGGGGCCGCAGTCCTCTACCCCTGCGTGGTGTACGA
                                                                                                                                                    GCGTGGTGTACGACTGTGGCCCCCAGCGCCTTGGAATAAAAATCCTCTTGCTGTTTGCA
ACTGCAATCTGTCACTCTGCCCAGGAGCCCACGCAGGATGCGGACCTCCGGAGCTATTTTA
                                            ----TIGIGATATITIGAAATGATIGGTITIGIAAAGCGCGGCCTTIGITGTGAACCCCA
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.larity 95.7%; Pred. No. 0;
Conservative 0; Mismatches 224; Indels 63;
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                                                                                                                                                                                                                                                                                                                                                                                                     agent; vaccine;
                                                                                                                                                                                                                                                                                                                                                                           env protein coding sequence SEQ ID
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                                                                                                                   TACGITIGCCICAGAICAGITATICCIAGICIGA-----CCICACCCCCAGAIAIC
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CAACGGCTGTGAAAGTCGAAGGAATCTCCACCTGGATCCATGCATCCCACGTTAAGCCGG
                                                                  TCCATCGCGTGGTTCCTTACTCTGTCAATAACCTCTCAGACTAATGGTATGCGCATAGGA
                                                                                                         GACAGCCTGAACTCCCATAAACCCTTATCTCTCACCTGGTTAATTACTGACTCCGGCACA
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                           CGCCACCTCCCGATTCGGGGTGGAAAGCCGAAAAGACTGAAAATCCCCTTAAGCTTCGCC
                                     6304 CGCCACCTCCCGATTCGGGGTGGAAAGCCGAAAAGACTGAAAATCCCCTTAAGCTTCGCC
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This sequence represents the putative coding regions for viral proteins

Taukuba-1 and contains the putative coding regions for viral proteins

Cand, PoL and ENV. This sequence and PCR fragments generated from the

sequence (see AAT74812-T74882) could be used to screen organs for porcine

retroviruses prior to xenotransplantation. Transplantation can increase

the likelihood of retroviral activation if intext and infectious

creproviruses are present. The porcine retroviral sequence can be used to

generate probes to determine the level (e.g. copy number) of intext (i.e.

potentially replicating) porcine provirus sequences in a strain of

contentially replicating operate provirus sequences in a strain of

contential sequence of activated retrovirus. Using Polymerase Chain Reaction DNA

contentiation (PDQ) on blood mononuclear cells, infectivity tirration and

susceptibility testing can be performed. Ultimately animal donors without

cintact porcine retroviral sequences or with a lower copy number of viral

clements could be selected. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid from porcine retro:viruses - used for detecting viruses in transplant or other tissue and for assessing risk of transmitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retrovirus; porcine; GAG protein; POL protein; ENV protein; xenotransplantation; infectious; provirus; organ transplant; donor; activated virus; Tsukuba-1; PCR; ss.
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                                                                                                                                                                                          AAT74811 standard; cDNA; 8060
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                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
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Best Local Similarity
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11-FEB-1998
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1, Conservative 0, Mismatches 10, Indels 5; Gaps 5  GGCTGGTGAACHTGGGCCCAACGGCGTTGGAATAAAATCCTTTGCTGTTTGCAACHTGTTTGCAACGGCTGGAATACAAAATCCTTTGCTGTTTTGCAACGGCTGTTTGCTGTTTTGCAACGGCTGGAATTCCAACGGCTGGAAGTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACAGGTTTTTAACATTTGCAGGATTCAACGGCTTTTTAACATTTGCAGGATTCAACAGGTTTTTAACATTTGCAGGATTCAACAGGTTTCAACAACAACACACAGTTTCAACAACAACAACACAGTTTCAACAACAACAACACACATTCAACAACAACAACAACA	1081 GAGCTCCGGCGGTGGAGCACCTGCAGGGACTCGGAGCCGAGGGGCCCCCCGG 1140	CTAACCATCCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGGAGTCCCTTA 13	CAGACACTCTTCACAA 3	68 GACCCACGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCCGGTTGGG 4 01 ACTACAACACGGCTGAAGGTAGGGAGAGCTTGAAAATCTATCGCCAGGCTCTGGTGGGG 1 1	1561 GTCTCGGGGGCCTCAAGACGCCCACTAATTTGGCTAAGGTAAGAGAGTGATGCAGG 1620	1681 CCCCTTTGATCCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCTTTATAGGAC 1740	1801 TACGTGATCTAGTGAAGGGGCAGAAAGTATATTACAAAAGGGAGCCAGAAGAAA 1860	1921 AGAAGAATTTGACTAAGATCTTGGCTGCAGTGGATGAAGGGAAAAGCAATACGGAAAGGG 1980	2041 CCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAAGAGACACTGGGCAAGGAACT 2100
1, Conservative 0, Mismatches 10, Indels 5, Gaps 5  GGCTGGTGAACHTGTGGCCCAACGCGTGGAATAAAATCCTTTGCTGTTTGCAACTGTTTCAACTTTTTTTT	> 6 8 8 8 8	ò a ò	8 8 8 8	ය <i>ද</i> ර සි	8 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	d d da	ò da ò da	8 8 8
	Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps   1 GCGTGGTGTACGACTGCGCGCGCTTGGAATAAAAATCTCTTTGCTGTTTGCA 6	40000 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3			481 CTTTTGCCTGCTTGTGGAAGACGTGGACCTGCTCGCTCTTGGTTTCTG 5	3068 TITIGIGIGICITIGICITIGICIGICICITIGICIACAGITITAAIA19GGGACAGACGGIGA  601 CGACCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGGCTCATAATT  3128 CGACCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGGCTCATAATT  661 TGTCAGTTCAGGTTAAGAAGGGACCTTGGCAGACTTTCTGTGTCTCTGAATGGCCGACAT  7.00 TTTCAGTTCAGGTTAAGAAGGGACCTTGGCAGACTTTCTGTGTCTCTGAATGGCCGACAT  7.00 TTTCAGTTCAGGTTAAGAAGAGAACCTTGGCAACTTCTGTGTCTCTGAATGGCCGACAT	11 TGGATGTTGGATGGCCATCAGAGGCCCTTTAATTCTGAGATTATCCTGCTGTTAAAG 78  721 TCGATGTTGGATGGCCATCAGAGGGACCTTTAATTCTGAGATTATCCTGGCTGTTAAAG 78  3248 TCGATGTTGGATGGCCATCAGAGGGACCTTTAATTCTGAGATTATCCTGGCTGTTAAAG 33  781 CAGTTATTTTCAGACTGGACCCTCCATCCCGATCAGGAGCCCTATACCTTAAGG 84	GGCAAGATTTTCAGACTGGGCCCCCCCCTCCCGAICAGGGCCCTAIATCCITACGI 33 GGCAAGATTTGGCAGAGGATCCCCGCCATGGGTTAAACCATGGCTGAATAAGCCAAGAA 90 GGCAAGATTTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATAAAGCAAGAAAAAAAA	961 AGCCTCTCCCCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGGAACCCCAT 102 961 AGCCCTCTCCTCATATCTACCCCGAGATTGAGGAACCCCGGCTTGGCCGGAACCCCAAT 102 3488 AGCCCTCTCCTCATATCTACCCCGAGATTGAGGAACCACCGGCTTGGCCGGAACCCCAAT 354 1021 CTGTTCCCCCACCCCTTATCTGGCACAGGGGGGGGGGGG

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121 TTTGCTGGTCTTACATTTGGGGGCTCGTCCGGGATCTGTCGCGGGCCACCCCTAACACCCCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a fragment thereof). The method is useful for RV detection and to assess graft transplantation risk. Screening of animals allows the elimination of donors with active replication of known viruses. Inactive proviruses can be detected and inactivated, allowing identification and elimination of potential human pathogens derived from swine in a manner not possible development of human corpuration. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2528 GCGIGGIGIACGACTGIGGCCCCAGCGCGCTIGGAATAAAAATCCTCTIGCTGTTIGCA
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            AGGAGGAGACTTGCAGATCCCACATCGTTTCCAAGTGGGAGATTCAGTCTACGTTAGACG
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                                                                                                                                                                                                                                                                                                                         transplantation; xenotransplantation;
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                                                                                            8045 CCACCGTGCAGGAAAC 8060
                                                                                                                                                                                                                                                                                                                                                           Porcine endogenous retrovirus.
                                                                                                                                                                                 AAF77725 standard; cDNA; 8060
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Best Local Similarity 99.7%;
Matches 5521; Conservative 0
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                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                        CCACCGTGCAGGAAAC
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CTAGAAGACTGGCAAGAGATAAAAAAGAGATAGACCA-TTCTCTGAGACTCCGGAAGGGACC
                                                                          TGCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAGAAGGGTTAGAATATGTCCAA
                                                                                                             AATACCTAAGGTAATAGGGTCAGACAATGGTCCAGCTTTTGTTGCCCCAGGTAAGTCAGGG
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                                                               TGCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAGAAGGGTTAGAATATGTCCAA
                                                                                                   C-AGATACATCGTCTAACCCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAACATC
                                                                                                                                       CCCTTATCATGTTCTGAGGCTACCAGGAGTGGCTGACTCGGTGGTCAAACATTGTGTGCC
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                            CTAGAAGACTGGCAAGAGATAAAAAAGATAGACCAGTTCTCTGAGACTCCGGAAGGGACC
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The invention relates to purified nucleic acid molecule that can specifically hybridise with the sequence of swine retroviruses. The nucleic acid is useful in methods for: determining the copy number or size of a porcine retrovirus from a human; screening a cell, tissue or a human being for the presence or expression of a porcine retrovirus or certoviral sequence; assessing the potential risk associated with the transplantation of a graft from a donor miniature swine or swine retrovirus or recipient animal or human; determining if an endogenous miniature swine or swine retrovirus or retroviral sequence genome includes a mutation that modulates its expression; providing a swine free of an endogenous retrovirus or retrovirus; localising the origin of a porcine retroviral infection; and inhibiting expression of an endogenous porcine retrovirus; and detecting a recombinant virus or other pathogens, e.g. protozoa or fungi. The present sequence represents porcine retrovirus; Tsukuba-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified nucleic acid molecules that specifically hybridize with swine retroviral sequences, useful for detecting the presence of porcine retrovirus, e.g., for assessing the potential risk associated with the
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                                                                                                                                                                                                                                                swine retrovirus; gene; virus; transplantation;
miniature swine retrovirus; porcine retroviral infection;
porcine retrovirus; Tsukuba-1; ss.
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The General Hospital Corporation; Boston, MA Location/Qualifiers

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   GTCACGGGACCACAGCAGCTAGAAACAGGACTTAGTAACCTACATCGAATTGTAACAGAA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                          1 (bases 1 to 8132)
Katyoshi, D.E., Denaro,M., Zhu,H., Greenstein,J.L., Banerjee,P. and
Fishman,J.A.
Identification of a full-length cDNA for an endogenous retrovirus
                                                                                                                                                          Fishman,J.A.
Direct Submission
Submitted (16-DEC-1997) Infectious Disease Unit, Massachusetts
General Hospital, 55 Fruit Street, Boston, MA 02114, USA
3 (bases 1 to 8132)
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Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts
Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts
General Hospiral, 55 Fruit Street, Boston, MA 02114, USA
Sequence update by submitter
On May 16, 1998 this sequence version replaced gi:3116441.
Location/Qualifiers
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                                                                                             of miniature swine 
J. Virol. 72 (5). 4503-4507 (1998). 
9557749
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Fishman, J.A.
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   TGTGTAGCCTTGAAGGAGGAATGCTGTTTTTATGTGGATCATTCAGGGGCCATCAGAGAC 7260
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                                                                                                                                                                                    99.9%; Score 8124; DB
larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Similarity
Matches 8127; Conserv
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| SGKOPGSILTHIRTRYPERATSSCWLCLALGPPYYEGWARRGKFNVYYREHRDQ CTWGSGONKITHISPSGICTMCGTWYOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOFTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTTWOTVOFFCOTT
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KKLMAVVEGRSATTERERDFRKIRSGFRQSGNLGNRTPLDKDQCAYCKERGHWARNCPK
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                                                                                             Chases 1 to 8132)
Fishman, J.A.
Direct Submission
Submitted (16-DEC-1997) Infectious Disease Unit, Massachusetts
General Hospital, 55 Fruit Street, Boston, MA 02114, USA
3 (bases 1 to 8132)
                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts General Hospital, 55 Fruit Street, Boston, MA 02114, USA Sequence update by submitter On May 16, 1998 this sequence version replaced gi:3116437.

Location/Qualifiers
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       (5), 4503-4507 (1998)
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/note="pol protein"
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miniature swine
Virol. 72 (5), 4
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Matches 8105, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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229 CAGITGAGITCCTGGTTGATACCGGAGCAACAITCGTGCTACTGCCATAGGAA 2288  2281 AACTAAAAGATAAAAAATCCTGGGTGATGGGTGCCACGGGCGACCACGGCCATAGGAA 2340  2282 AACTAAAAGATAAAAAATCCTGGGTGATGGGTGCCACGGGCCACCACGGTATCCATGGA 2340  2341 CTACCCGAAGAACATGACTTGGGAGTGGTGACCACCCACTCGTTTCTGGTCATGA 2341  2342 CTACCCGAAGAACACGTTGACTTGGGAGTGGGGCAACCACCGTTTCTGGTCATAC 2400  2348 CTACCCGAAGAACACGTTGACTTGGGAGTGGGGCGAACCCACTCGTTTCTGGTCATAC 2406  2407 CTGAGTGCCCAGCACCCCTTTAGGTAGACACACTATTGACCAACTTTCTGGTCATAC 2406  2407 CTGAGTGCCCAGCACCCCTTTAGGTAGACATATTGACCAAGATTGACAAATTT 2466  2407 CTGAGTGCCCAGCACCCTTTAGGTAGACAATATTGACCAAGATGGGAGCACAAATTT 2466  2407 CTGAGTGCCCAGGAACCAGAAGTGTCTGCAAAAATTT 2466  2407 CTGAGTGCCCAGGCACCCTTTAGGTAGAACTTATTGACCAAGATGGGAGCACAAATTT 2466  2407 CTGAGTGCCCAAGAACCAGAAGTGTCTGCAAAAAAACCCAAGATGGAGACCAAATTT 2466  251 CTTTTGAACAGGGAAACCAGAAGTGTCTGCAAAAAAACCCAAGATGACAAAAATATC 2580  252 TCCAATTAGATGACGAAATTCCACTATACTCTCCCCTAGTAAAAAATATAC 2580  252 TCCAATTAGATGACGAAATTCCACTATACTCTCCCCTAGTAAAAAATATAC 2580  251 AATTCTGGTTGGAACAGATATCCACAAGCTGGCCAAGAGTGGGTTGGCAA 2640  261 AATTCTGGTTGGAACAGTTATTCCACTATACTCTCCCCTAGTAAAAAATATAC 2580  261 AATTCTGGTTGGAACAGTTATTCCACTAGACACAGAACCGAACGGATCGGTTGGCAA  261 AATTCTGGTTGGAACAGTTATTCCACTAGACACAGAACCCTGATCAAAAAATACC 2700  261 AGCACCCCTTGAGTAAAGAAGCTCAAGAACCCACAGATCAGATCAGACACAGAACACCCAAGAGTTGGTAAAATATCCACAAGATTATTCAAACTGAAGCCAGAACCCAAGATTAAATCCACAAGAATTCAACAAGAACCCAAGAACCAACAAAAACCCAAAAAAACCAAAAAA	2167 AACAGGCATCCTAGTTCCTGTCTTTTTTTTTTTTTTTTT
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8
AGCGGACCAGACGACATTACCGCTGCGCACGTACGGCCCTCCCCACCGGGGGGGG	1681   CCCCTTTGATCCCACCTCAGAGGCCCAAAAGCCTTGGCCTTTTTAGCCTTTTTATAGGAGCCCCAAAAGCCTCAGTGGCTTTTTAGCCTTTTAGAGGAGCCCCAAAAGCCTCAGTGGAGGCTTAGGCCTTTATAGGAGCCCAAAAGCCTCAGTGGAGGCTTACAGGAGGCTTAGTGGAGGCTTAGTGTTTAGTAAAGAAGCCTCAGAGGCTTACAGGAGGCTTACAGGAGGCTTAGTTTAGTAAAGAAAG

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KQVPPOVI OLKASA TEVY KQYPLSKERAQEGI RPHYORLI OGGI LIVEVOSPMYTPLLE
VRKEGTNDYRPVQDLEGVKRYQDI HPTVPNPYNLLCALPPORSWYTVLDIKDAPFCL
RLHPFSQELPRERENDPGTGARTQGLTWATEVERPOSPMYTT DANS TO SHE
BENAMEDROAD FOR STALLSE BENGTRADILELESDLGKRASAKKQI CRREVYTLGYSLR
DGQRMLTEARKKTVVO I PAPTTAKQMR EFLGTAGFCRLM I DGFATLAAPLYPLTKEKG
EFSWAREPHQAKAPADA IKKALLSA PARALALDOYTKP FTLYVDERKCHYORCVITOTILGPWRR
PVALLSKKLDPVASGWP I CICKA LAAVA I LVKDADKLTLGQWITVI APHALEM I VRQPP
BNWMTNARWHYQSLLLTERVTFAPPAALNPATLLEGGWITTI NASSENEGTSAOKAELIM
KOLTOIP BLGESTLTWFTDGSSYVDEGKRAMAANVODTITI NASSENEGTSAOKAELIM
ALTQALRIAGKSI NI YTDSRYA PATAHVHQA I YKQRGLLTSAGRE IKWKEETLISLLE
AVHLDRRAATI HCCGHQKAKOLI SRGNQMADRVAKQAAQGVNLLP I I EMPKAPEPRRQ
YTLERMOEIKKLI DGYSETPEGTYTSOGREL VVQOLINGSHENOVETEVK
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PVALOSGGLAALI LGTUWKLACYPROGGEL TWOTICASHQCAHWWVDFTEVK
PVAKYGNKYLLOTYPGGWVEAVYROSSGOVERNMRT I KETLITATAFTGNOM IALL
PVALFRVRNTPGGFGLTPYELLYGGPPPLVBI ASSUSADVLLAGOPLESELKÄLEWWVE
GI PTWI HASHVKRAPPPPDSGWKEEKTENDLKLRHRVVPYSVNNSSS"
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rppDVLRAYGFYUCPGPPNNESYCGNPQDFCKQWSCVTSNDGNWKWPYSQDDRVSY
rppDVLRAYGGGRQPGSILTITRLKINDLEPPNALGPTLTGGRPPTGGNBIL
KWNNGMRGWAYTGYGGGRQPGSILTITRLKINDLEPPNALGPTLTGGRPPTGGPGS
SNITSGSDPTESNSTTKMGSQNKLTLTEVSGKGTCIGKVPPSHQHLCNHTEAFNQTSE
SQYLVPGYDRWMGATGLTPCVSTLVFNQTTCDFCIMOVIVPRIYY YP ERALIDEY DYR
NHRQKREPISLTLAVMLGLGVAAGVGTGTAALVTGPQOLETGLSNLHRI VTEDLGALE
KSYSNLEESITSLSEVVLQORRGEDDLAFLKEGGELCVALKEECCFYVDHSGAIRDSMSK
LRERLEKRREKETTCGWRGANGSPUNDLATLLSALTGPLIVLLLTVGPCIINKLI
                                                                                                                                                                                                                     RKKVPGADGRPTOLONEIDNGFPLTRPGMDYNTAEGRESLKITRQALVAGLRGASRRP
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EQGKPEVSANNKPITVLTLQLDDEYRLYSPLVKPDQNIQFWLEGFPQAWAETAGMGLA
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                                                                                                                                                                                                                                                                                                                                                                                              /note="suppressed stop codon between gag and pol"
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0; Mismatches 138; Indels
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97.7%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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Best Local Similarity 97.7
Matches 7984; Conservative
                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group.
1 (bases 1 to 8188)
Bartosch, B., Stefanidis, D., Myers, R., Weiss, R., Patience, C. and
     7686 TGCTGTTTTAAAATATGCGGAAGTAAAATAGGCCCTGAGTACATGTCTCTAGGCATGAAA 7745
                                                                                                                                                                                                                                    7806 GTAAAACTGGTTGCGCCATAAAGATGTTGAAACATGTTGATACACATATCTTGGTGACAACA 7865
                                                                                                                                                                                                                                                                                               TGTCTCCCCCACCCGGAAACATGCGCAAATGTGTAACTCTAAAACAATTTAAATTG 7918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRL 26-NOV-2004
                                                                                                             CTTCTTGAAACTATTTGAGATAACAAGAAAAGGGAGTTTCTAACTGCTTGTTTAGCTTCT 7805
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8188 bp DNA linear VRL 26-NOV-200 Porcine endogenous retrovirus C/A gag protein gene, complete cds; pol protein gene, partial cds; and env protein gene, complete cds.
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/country="United Kingdom"
/note="high-titer, human-tropic PERV subgroup C/A
recombinant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (Dases 1 to 8188)
2 (Dases 1 to 8188)
Bartosch, B., Patience, C., Weiss, R. and Takeuchi, Y.
Bartosch, B., Patience, C., Weiss, R. and Takeuchi, Y.
Burnitted (11-MAR-2004) Wohl Virion Centre, Windeyer Institute,
UCL, 46 Cleveland Str, London WIT4JF, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7926 Griccacgaagcgcgggcriccgaagririaaarirgacrggrirgrgararirrgaaarga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGGTTTGTAAAGCGCGCGCCTTTGTTGTGAACCCCCATAAAAGCTGTCCCGACTCCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCACGAAGCGCGCGCGCTCTCGAAGTTTAAATTGACTGGTTTGTGATATTTTGAAATGA
                                                                                                                                                                                  7799 GTAAAACTGGTTGCGCCATAAAGATGTTGAAATGTTGATACACATATCTTGGTGACAACA
                                                                    CTICITGAAACTATTTGAGATAACAAGAAAAGGGAGTTTCTAACTGCTTGTTTAGCTTCT
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Evidence and Consequence of Porcine Endogenous Retrovirus Recombination
J. Virol. 78 (24), 13880-13890 (2004)

    .8188
/organism="Porcine endogenous retrovirus C/A"

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AUTHORS
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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porcine endogenous retrovirus C/A

(SM Porcine endogenous retrovirus C/A

Viruses, Retro-transcribing viruses, Retroviridae,

Viruses, Retro-transcribing viruses, Retroviridae,

Viruses, Retro-transcribing viruses, Retroviridae,

Viruses, Retro-transcribing viruses, Retroviridae,

SE Denner, J., Karlas, A. and Votteler, Jr.

Nucleotide sequence and extended characterization of a high passage human cell-adapted recombinant PERV-C/A

AL Unpublished

CE (bases 1 to 8305)

RS Denner, J., Karlas, A. and Votteler, Jr.

Direct Submission

Submitted (04-WAR-2005)

Direct Submission

Submitted (14-WAR-2005)

Direct Submission

D-13353, Germany

CE DIRECT 20, Berlin
                                                                                                                                                                                                                                                                                                                      AY953542

Porcine endogenous retrovirus C/A isolate C/A 4 gag protein (gag), pol protein (pol), and envelope glycoprotein (env) genes, complete
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/isolation source="Homo sapiens 293 cells infected with
/isolation source="Homo sapiens, FDA"
/isolation source="Homo sapiens"
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6658 GAGGITTCTG 	6781 AACCACACTG	6841 GGGTGGTGG	6901 ACTAAAGACT	6898 GCAATCCTTC	7021 ACACTAGCTC	7081 CTAATCACAC	7141 GAAGATCTCC	7201 TCTGAAGTG		7258 GACTCCATG 	7381 CAAGGGTGG	7441 TTAACAGGA		7498 CAGTACCAA          7561 CAGTACCAA	7558 AACTATTAA          7621 AACTATTAA	7681 GAACCCAGG	7741 AGGTAAAAG
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116	GGCTCATAATTTGTCAGTTAAGAAGGGACCTTGGCAGACTTTCTGTGTCTCTGA  GGCTCATAATTTGTCAGTTCAGGTTAAGAAGGGACCTTTGGCAGACTTTCTGTGTCTCTGA  ATGGCCGACATTGTCAGTTCAGGTTAAGAAGGGACCTTTGGCAGATTATCTGTGATTATCTTGTCTTGTTTTTTCAGATTGCCATCAGAGGGAACCTTTAATTCTGAGATTATCTTGTCTTTTTTTT
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id="CAC39616.1"
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Comparison of replication-competent molecular clones of porcine
endogenous retrovirus class A and class B derived from pig and
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Submitted (31-JUL-2000) Toenjes R.R., Medical Biotechnology,
Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 51-95, Langen, 63225,
                                                                                                -----GGAAGTAAAATAGGCCCTGAGTACATGTCTCTAGGCATGA
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polymerase; polyprotein.
Pordine endogenous type C retrovirus
Pordine endogenous type C retrovirus
Viruses; Retro-transcribing viruses; Retroviridae;

    .8918
/organism="Porcine endogenous type C retrovirus"

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/mol_type="genomic DNA"
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MESTRICAL SEQUENCE 3 from Parent MOD2072336. BM linear PAT 26-NOV-2002 BM MCCESSING MASSACRAD ACCESSING MASSACRAD ACCESSION AC	TCGAGGGCCCACATTCCANGTTCAGGTAAAGAGGGCCCTTGGCAGACTTCTGTGCCCTTTAATTCTGAGTTTCAGTTTGAATGCCCACAGGGGCCCTTTAATTCTGAGTTTCAGTTTGAATGCCCACAGGGGCCCTTTAATTCTGAGATTTCTGAATGCCCCACAGAGGGCCCCTTTAATTCTTGAGATTTCTGAATGCCCACAGAGGGCCCTTTAATTCTTGAGATTTCTGAGATTTTTTCCAAGAGGGCCCCTTTAATTCTTGAGATTTTTTCTGAAGGGCCCCCTTTAATTCTTGAGATTTTTTCCAAGAGGGCCCCCGCCTTTAATTCTTGAGATTTTTTCTCAAGAGGGCCCCCTTTAATTCTTGAGATTTTTTCCAAGAGGGCCCCCCTTTAATTCTTGAGATTTTTTCCAAGAGGGCCCCCGCTTTCAATTCTTGAGAGATTTTTTTCCAAGAGATTCTTCCCCCACTCCAGGGGTTAAACCATTGAGCCAAGATTTTTTTCCCCCCCC	2113 ĊAĠĠĊTĊŦĠĠŦĠĠĠĠŦĊŦĊĊĠĠĠĠĠĊŦĊĀĀĠĀĊĠĊĊĊĀĊŢĀĀĊŢŦĠĠĊŦĀĀĠŦĀ 2172 1605 AGAGAĀGTGĀTGGĀCGGĀĀTGĀĀCCCCTCŢĢŢŢŢŢŢŢŢŢĠĀĠĠĠŢĊŢŦĠĠĀĀ 2172 11605 AGAGĀGGĀTGĀĀGĀĀCGĀĀTGĀĀCCCCTCŢĢŢŢŢŢŢŢŢŢĠĀĠĀĠĠŢĊŢŢĠĠĀĀ 2232 11665 GCCŢŢĊĀĠĠĠĠŢĀCĀCCCCŢŢŢŢĠŢĠCCCŢŢŢĠĀĠĀĠĠĊŢĊĀŢĠĠĀĀ 2232 11665 GCCŢŢĊĀĠĠĠĠŢĀCĀCCCCŢŢŢŢĠŢĠCCCŢŢŢĠĀĠĠĠĊŢĊĀĠĠĀĀ 2232 1233 ĠCCŢŢĊĀĠĠĠĠŢŢĊĀĊCCCŢŢŢŢĠŢĊĊĀĠĀĠĠĊŢĊĀĀĠĠĠŢŢŢŢŢŢŢŢŢŢ
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HUICEUR BEAR EN Z NOU	AX546209  Sequence 3 from Patent W02072836.  AX546209.  AX546209.1 GI:25811408  Pig endogenous retrovirus Tornicae; Retro-transaczibing viruses; Retroviridae; Orthoretrovirinae; Gammaretrovirus.  Replication-competent molecular clones of porcine endogen retrovirus class a and class b derived from pig and human Patent: W0 02072836-A 3 19-8EP-2002; Peul-Ehrlich-Instituts; Prof Dr Johannes Loewer (DE) Localion/Qualifers Nonle-Emrinding primary fibroblasts Anole-Emrinding primary fibroblasts Anole-Emrinding primary fibroblasts Anole-Emrinding Conservative Anole-Emrinding Conservative Anole-Emrinding Conservative In Gorthage Conservative In Hill	CGGGGCCGTCCGACTCTTTTGCCTGCTTGTGAAACGCGAACGGGTCGTGTGTGT

	CCTGACGTCACAACCCTTTACCCTTTATGTGGGTGGGGGGGG
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23	### ATCACTGTGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGG

S505 GTCTAGGTAGACGCCACCGGGGAAACC  5070 GTCTATGTAGACGCCACCGTGCAGGAAACC  5056 GTACTTTGACCACCACCGGGGTGTGAAAG  6130 GTACTTTTGACCACCACGGGTGTGAAAG  5025 TCCCACGTTAAACCTGCGCCCCCTTCCGATT  6190 TTCCACGTTAAACCTGCCTCCATCGGTGTTC  5085 CCCTTAAAGCTTCGCCTCCATCGGTGGTTC  5745 TGGTATGCGCTTGGCGTGCTGGTGTTC  5310 TGGTAGCTCGCTTGTGGACACCCCTCCATCGGTGGTTC  5805 TACTGACTCGGCTTGTGGACACTCCGTGGTTC  5805 TACTGACTCGGCTAGGTATTAATATAACCC  5805 TACTGACTCGGCTAGGTATTAATATAACC  5805 TACTGACTCGGCTATGTGGTTAATATAACCC  5805 TACTGACTCGGCTATGTGGCTTCACGGT  6430 CTGGTGGCCTGATTAATATTTAAC  5805 TACTGACTCGGCAATTAATATTAACC  6076 TACTGACTCGGCAATATATATTACCCTCACGA  5806 TACTGACTCGGCAATATATATTAACCTCACGGA  6430 CTGGTGGCCCTGATTAATATTAACGGTTCGCTTCGCT  6036 TAATGATGGGGAATTCCTCCATGGGTTTCACGGG  6036 TAATGATGGGAAAATTCCTCAGGATTTTAAC  6036 TAATGATGGGAAATTCCTCCAGGATTTTAATATAATATTAAC  6036 TAATGATGGGAAATTCCTCCAGGATTTTAATATTAATATTAATATTAACTCTCTCAGGATTTTCTCGAAAATTTAATATTAATATTAATATTAATATTAACGGTTTCTTCTTCTTCTTCTTTCT	686868686868686	CATCAGAAAGCTAAAAGATCTCATATCCAGAGGAAACCAGATGGCTGACCGGGTTGCCAAG CATCAGAAAGCCCAAAGATCCCATATCCAGAGGGAACCAGATGCTGACCGGGTTGCCAAG CAGGCAGCCCAGGGTTAACCTTCTGCCTATAATAGAAATGGCTGACCGGGTTGCCAGA CAGGCAGCCCAGGGTTAACCTTCTGCCTATAATAGAAATGGCCCCAAAGCCCCAGAACCC CAGGCAGCCCAGGGTTAACCTTCTGCCTATAATAGAAATGGCCCCAAAGCCCCAGAACCC CAGGCAGCCCAGGAAGACTGGCAAGAAATAAAAAAAAAA
	6666	AAACATTGTGTGCCCTGCCAGGTGATAATGCTAATCCTTCCAGAATGCCTCCAGGGAAG
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6310 TGGTAAACGCCTTGTGGACAGCCCGAACTC 5805 TACTGACTCCGGCACAGGTATTAATATCAA	a 8	TTAGAATATGTCCAACAGATACATCGTCTAACCCCCCCTAGGAACTAAACACCTGCAGCAG 
6250 ccccrraadcrricdccrccarcegrafric 5745 regrangegeanageagacagecrgaacrc	<u>ብ</u> ጵ	ACTCCGGAGGGACCTGCTATACCTCAGATGGGAAGGAATCCTGCCCCACAAAGAAGGG
5685 CCCTTAAGCTTCGCCTCCATCGCGTGGTT	ò	GGACGACAGTACACCCTAGAAGACTGGCAAGAATAAAAAAGATAGACCAGTTCTCTGAA ACTCCGGAAGGGACCTGCTATACCTCAGATGGGAAGGAATCCTGCCCCACAAAGAAGG
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6130 GTACTTTGACCACACCAACGGCTGTGAAA	: A &	CAGGCAGCCCAGGGTGTTAACCTTCTGCCTATAATAGAAATGCCCAAAGCCCCAGAACCC
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	8	CTAAGCCTATTAGAAGCCTTACATTTGCCAAAAAGGCTAGCTA
5445 GAGGCCTACTCAGGAGGAGGAGGACTTGCAGA.	දි සි	CTAAGCCTATTAGAAGCCGTACATTTACCAAAAAGGCTAGCTA
5385 TTGTTCTTGGGTCAAGGCACTTGAGTGGGTCAGGTGGGTCAGGTGGGTCAAGGCGCTCGAGGCGCTCGAGTGGGGTCAAGGCGCTCGAGTGGGG	රි සි	4305 TATAAACAAAGGGGTTGCTTACCTCAGCAGGGGAAATAAAGAACAAAGAAGAAATT 4364 
е п	qa	4245 ATAAACATTTATACGGACAGCAGGTATGCCTTTGCGACTGCACGTACATGGGGCCATC 4304 
	8 è	4185 GCACAAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTGCGGCTGGCCCAAGGAAATCC 4244
5773 AATTGACCACAGAGACTGGCATTAATGATTIIII 5265 AGGGTTAGGAACACCCCTGGACAGTTGGGC	<u>육</u> &	4123 GCGCCGGTGGACCGCACCACCATCTGGGCCAGCAGCTGCCGGAAGGAA
	8 &	GIGTTAACCTGGTTCACTGACGGAAGCTGTTTTTTTTTTT
5145 AGACCCAAAGCTCAGGACAGGTAGAGAGGA 	ð <del>f</del>	GIGGTRACCTGGTACACTGCTGACGGCTGATGTGGTGGAAGGTAAGGGGTGGCGCTGGTGAAGGTAAGGGGTAAGGGGTGAGGTGAGGTGAAGGTAAGGGGTAAGGGGTGAGGTAAGGGGTGAGGAAGGAAGAA
າ ຕ	g 48	4005 CTATTGATTGAGGAGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAA 4064 [
	<u>a</u> a	3945 AACCCTGCCACTCTTCTGCCTGAAGAGACTGATGAACCAGTGACTCATGATTGCCATCAA 4004

5832 5892 6129 6189 5915 TCAGCAGGATAGGGTAAGTTTTCTTATGT 6095 5772 5952 6012 5564 5624 TCGGGGTGGAAAGCCGAAAAGACTGAAAT 5684 CCTTACTCTGTCAATAACCTCTCAGACTAA 5744 CCATAAACCCTTATCTCTCACCTGGTTAAT 5804 ATTIATGCCCAGGACCACCAATAA 5975 CTITIGIAAACAAIGGAACIGIGIAACCIC 6035 TTACCTGACCTGGATTAGAACTGGAAGCCC 6155 5144 5264 5324 5384 5444 ATCCCACATCGTTTCCAAGTGGGAGATTCA 5504 CAACACTCAAGGGGGGCTCCTTTAGGAAC 5864 ATGAATAGAACCATTAAAGAGACCCTTACT CATAGIGCTGAGGTGCTTTCCCAGCCT CTCGAGACTCGGTGGAAGGGACCTTATCTC ATCAGTTATTCCTAGTCT-----GAC CTCGAGACTCGGTGGAAGGGCCCTTATCTC

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GINDWIALLPFVLFRVRNTPGQFGLTPYELLYGGPPPLAEIAFAHSADVLLSQPLFSR
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TIPTAVKVEGIPTWIHAFHVKPAPPSDSGWKAQKTENPLKLRLHRVVPYSVNNSSS"
6185. 18149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 GATTITAACTCGACTGGCCTTTCAGTTTGGTGCGTTGGCCGGGAAACCCGCGACTACCCC 738
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; Pred. No. 0;
0; Mismatches 5
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/gene="env"
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Best Local Similarity 91.0
Matches 7543; Conservative
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ADLYNWKTNHPPFSEDPORLTGLVESLMFSHOPTWDDCQQLLQTLFTTEERRILLEA
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KILAAVVEGKSNRERBERRDFRKIRSGPRQSGNLGNRTPLDKDQCAYCKEKGHWARDCPK
                                                                                                                                                        PEN279056 8918 bp DNA linear VRL 15-APR-2005
Porcine endogenous retrovirus proviral gag gene, pol gene and env
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Viruses, Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group.
                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Czauderna, F., Fischer, N., Boller, K., Kurth, R. and Tonjes, R.R. Establishment and characterization of molecular clones of porcine endogenous retroviruses replicating on human cells J. Virol. 74 (9), 4028-4038 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niebert, M., Rogel-Gaillard, C., Chardon, P. and Tonjes, R.R. Characterization of chromosomally assigned replication-competent gamma porcine endogenous retroviruses derived from a large white pig and expression in human cells J. Virol. 76 (6), 2714-2720 (2002)
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Submitted (12-SEP-2000) Toenjes R.R., Medical Biotechnology,
Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 51-95, Langen, 63225,
                                                                                                                                                                                                                                                                                                                                     AJ279056.1 GI:18076256
env gene; env protein; gag gene; group specific antigen; pol
pol protein.
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/function="retroviral protease and polymerase"
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/organism="Porcine endogenous retrovirus"
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/spe_ific host="Sus scrofa"
/db_xref="taxon:61673"
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/gene="gag"
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/gene="pol"
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/mol type="genomic DNA"
/strain="type C"
/db xref="taxon:61673"
/clone="42"
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/note="gly4"
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TAAGCTTACCCTTACTGAGGTTTCTGGAAAAGCACCTGCATAGGGATGGTTCCCCCATC 7329
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Porcine endogenous retrovirus type C proviral gag, pol and env AJ133817 8648 8708 8114 7994 8054 8469 TAAGATAAAAGAGGAGAAGTCAATTGCCTAACGGACCCCAGTAAGATCGGGCGTGCAC 8528 Porcine endogenous retrovirus
Porcine endogenous retrovirus
Porcine endogenous retrovirus
Voiruses; Retro-transcribing viruses; Retro-transcribing viruses;
Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group. CTCGAAGTTTTGAATTGACTGGTTTGCGATATTTTAAAAATGATTAGTTTGTAAAAAGCGC 8709 GGGCTTTGTTGTGAAACCCCATAAAAGCTGTCCCGACTCCACACTCGGGGCCGCAGTCCTC CTATTTGAG GGGCTTTGTTGTGAACCCCATAAAAGCTGTCCCGACTCCACACTCGGGGCCGCAGTCCTC AAAGATGTTGAAATGTTGATACACATATCTTGGTGACAACATGTCTCCCCCACCCCGAAA CTCGAAGTTTTAAATTGACTGGTTTGTGATATTTT-GAAATGATTGGTTTGT-AAAGCGC CATGCGCAAATGTGTAAACTTCTAAAATTT-AAATTAATTGGTCCACGAAGCGCGGGCT Submitted (04-MAY-1999) Toenjes R.R., Wedical Biotechnology, Paul-Ehrlich-Tastfuut, Paul-Ehrlich-Strasse 51-59, Hessen, I Langen, GERMANY Б /note="grown in PK15 (ATCC No. CCL-33) cell line"
1. .668
506 AJ133817.1 GI:6688947 env gene; env protein; gag gene; gag protein; pol gene; protein. Kurth, R. Toenjes,R.R. Molecular Characterization of Human-tropic and Replication-competent Porcine Endogenous Retroviruses Location/Qualifiers 1. .8849 /organism="Porcine endogenous retrovirus" Krach, U.,

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/ protein ideache=
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/ db_xref="G1:668948"
/ db_xref="InterPro:IPR000223"
/ db_xref="InterPro:IPR000477"
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VLQNRRGLDLLFLKEGGLCVALKEBCCFYVDHSGAIRDSMSKLRERLERRRREREAD
GWFEGWFNRSPWMTTLLSALTGPLVVLLLLLTVGPCLINRFVAFVRERVSAVQIMVLR
QQYQGLLSQGETDL"
Joan(1115. .2686,2690. .6271,6150. .8132)
/note="unnamed protein product; viral polypeptide"
/codon_start=1
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/gene="agg"
/product="agg protein"
/citation="retroviral capsid"
/citation=[1]

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/function="retroviral protease and polymerase"
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/gene="gag"
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/gene="pol"
6150. .8129
/gene="env"
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                                                                                                     GCGTGGTGTACGACTGTGGGCCCCCAGCGCGTTGGAATAAAAATCCTCTTGCTGTTTGCA
                                                                                    Gaps
                                                                Length 8849
                                                                                   693; Indels 128;
                                                                    13;
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8182. .8849
8742. .8747
                                                                    8
                                                                                    0; Mismatches
                                                                   Score 6746.2;
Pred. No. 0;
                                                                   83.0%;
90.0%;
                                                                    Query Match
Best Local Similarity 90.0
Matches 7430; Conservative
                                 polyA_signal
ORIGIN
mat peptide
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/product="gag-pol polyprotein"
/protein id="AAM29192.1"
/db xref="G1:21064961"
/db xref="G1:21064961"
rianslation="MGQTVTFLSLTLDHWTEVRSRAHNLSVQVKKGPWQTPCASEWP
TPDVGWPSEGTFNSTILAYVALIFOTGPGSHPDOEPYILTWODLAEDPPWVKPWLN
KPRKPGPRILALGEKNKHSAEKVEPSPRIYPEIEEPPTWPEPQPPPPAQGAVRG
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ADLYNWKTNHPPFSEDPQRLTGLVESLMFSHQPTWDDCQQLLQTLFTTEERERILLEA
RKNVPGADGRPTQLQNEIDWGFPLTRPGWDYNTAEGRESLKIYRQALVAGLRGASRRP
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DLQALEKSVSNLEESLTSLSEVVLQNRRGLDLLFLKEGGLCVALKEECCFYVDHSGAI
RDSMSKLRERLERRRREREADQGWFEGWFNRSPWMTTLLSALTGPLVVLLLLLTVGPC
LINRFVAFVRERVSAVQIMVLRQQYQGLLSQGETDL"
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ALLPFVLFRVRNTPGQFGLTPYELLYGGPPPLABIAFAHSADVLLSQPLFSRLKALEW
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KVBGIPTWIHASHVKPAPPPDSGWKAEKTENPLKLRLHRVVPYSVNNSSS"
                                                                                                                                                                                                cells infected with PERV from
Bartosch, B., Weiss, R.A. and Takeuchi, Y.
Direct Submission
Submitted (23-AFR-2002) Wohl Virion Centre, Windeyer Institute, UCL, 46 Cleveland St, London W174JF, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6727; DB 13; Length 8714;
Pred. No. 0;
0; Mismatches 695; Indels 131; Gaps
                                                                                                               ¥
                                                                                                                     /organism="Porcine endogenous retrovirus
                                                                                                                                                                                                                                                                                                                                           except=(pog:2585. .2587,aa:OTHER)
                                                                                                                                                                                                /isolation_source="human 293 cells infeporcine PK-15 cell supernatant"
/db_xref="taxon:194958"
569. .586
1013. .6169
/note="internal stop codon suppressed"
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/product="env protein"
/protein_id="AAM29191.1"
/db_xref="G1:21064960"
                                                                                                                                                             /mol type="genomic DNA"
/isolate="PERV-60"
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Best Local Similarity 90.0%;
Matches 7425; Conservative
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Porcine endogenous retrovirus A gag-pol polyprotein and env protein
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Orthoretrovirinae, Gammaretrovirus; 1-Mammalian type C virus group.
1 (bases 1 to 8714)
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PCR-based cloning and immunocytological titration of infectious porcine endogenous retrovirus subgroup A and B
J. Gen. Virol. 83 (Pt 9), 2231-2240 (2002)
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                                                                                                         CTTAGACAACAGTACCAAAGCCCGTCTAGC---AGGGAAGCTGGCCGCTAGCTCTACCAG
                                                                                                                            7546 TICTAAGATTAGAACTATTAACAAGAGAAGAAGGGGGGAATGAAAGGATGAAAATACAAC
                                                                                                                                                                                                          AAACATGCGCAAA---TGTGTAACTCTAAAACAATTTAAATTAATTGGTCCACGAAGCGC
                            7429 ATTATTAACAAGTTAATTGCCTTCATTAGAGAACGAATAAGTGCAGTCCAGATCATGGTA
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                       TITGITCCTT-----ATAGGTAAAAGATTAGGTTTTTTGCTGTTTTAAAATATGCGG
                                                                                                                     AACTGACTGGCACCATAGAAGAATTGATTACACATTGACAGCCCTAGTGACCTATCTCAA
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TTCTAAGATTAGAACTATTAACAAGACAAGAAGTGGGGGAATGAAAGGATGAAAATGCAAC
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Pred. No. 0;
0; Mismatches
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Methods to inhibit infectious agent a xenotransplantation
Patent: WO 0071726-A 23 30-NOV-2000;
Mayo Medical Ventures (US)
Location/Qualifiers
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WO0071726.
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Seguence 23 from Patent 1
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Similarity 91.4%;
7; Conservative
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| /mol_type="genomic DNA" |
| /solate="bac-PERV-A(151B10)" |
| /solate="bac-PERV-A(151B10)" |
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Viruses, Retro-transcribing viruses, Retroviridae,
Othoretroviruae, Gammaretrovirus, 1-Mammalian type C virus group.
1 (bases 1 to 811)
Niebert,M., Rogel-Gaillard,C., Chardon,P. and Tonjes,R.R.
Characterization of chromosomally assigned replication-competent
gamma porcine endogenous retroviruses derived from a large white
pig and expression in human cells
10 Virol. 76 (6), 2714-2720 (2002)
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Niebert, M., Rogel-Gaillard, C., Chardon, P. and Toenjes, R.R.
Direct Submission
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            CTACATCGAATTGTAACAGAAGATCTCCAAGCCCTAGAAAAATCTGTCAGTAACCTGGAG
                                   GAATCCCTAACCTCCTTATCTGAAGTAGTCCTACAGAATAGAAGAGGGTTAGATTTATTA
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larity 88.7%; Pred. No. 0;
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Best Local Simil
Matches 7357; (
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1313   TGATCOMANTACCANTTOGGGTGGACACATTTCCCAAGCCTTGGCGCGCGCGC 2866   1315   GATGGGTTTGGCAAGTTCCCCCCAAGTTATTCAACTGAAGCCCAAGTTGCCCCCCCC
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7939 CGAAGTTTTAAATTGACTGGTTTGTGATATTTGAAATGATTGGTTTGT-AAAGGGG 7995	8643 CGAGTITGGAATTGACTGGTTTGCGATATTTTTAAAAATGATTAGTTTGTAAAAGCGCG 8702	7996 GGCTITGTTGTGAACCCCATAAAAGCTGTCCCGACTCCACACTCGGGGCCGCAGTCCTCT 8055	8703 GGCTTTGTTGTGGAACCCCATAAAAGCTGTCCCGACTCCACACTCGGGGCCGCAGTCCTCT 8762	8056 ACCCCTGCGTGGTACGACTGTGGGCCCCAGCGCGCTTGGATAAAATCCTCTTGCTG 8115	8763 ACCCCTGCGTGGCGTACGACTGTGGGCCCCCAGCGCGCTCGGAATAAAATCCTCTTGCTG 8822	8116 TTTGCATCAAAA 8127	8823 TTTGCATCAAGA 8834
CGAAGT	CGAAGT	GGCTTT	GGCTTT	ACCCCT	ACCCCT	TTTGCA	TTTGCA.
7939	8643	7996	8703	8056	8763	8116	8823
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Search completed: February 4, 2006, 23:52:44 Job time : 26242 secs

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                CN156883 943991 MA
BW960748 BW960748
CF181622 B18471 MA
CN154477 941687 MA
BP158726 BP158726
DN118990 1118819 M
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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CF360188 821495 MA
DN113185 1112434 M
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Mus musculus embryo RCB-0549 Cle-H3 cDNA, RIKEN full-length enriched library, clone:G431002112 product:gene el protein, full
DN113535
DN12276
DN122276
CF180285
DN118659
AJ747000
CF178916
DN122183
CN1223467
CJ010874
AK014027
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
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he RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

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8 Result

TITLE JOURNAL REFERENCE AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

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L Submitted (16-APR-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (B-mail.genome-resegner.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, CMA.library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

IN Nature 420, 563-573 (2002)

S Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imctani, K., Ishii, Y., Itoh, M., Kawai, I., Kawai, J., Kojima, Y., Konno, H., Konno, H., Kouda, M., Kawai, J., Kavai, J., Kohima, Y., Konno, H., Konno, H., Konda, M., Nashi, K., Nomura, K., Numzazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Sait
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/ Organism=Mus musculus"
/mol type="mcNN DB:G431002112"
/db_xref="texcn:10090"
/clone="G431002112"
/cell_line="RCB-0549 Cle-H3"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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LTGEEKQRVLLEARKAVRGNDGRPTQLPNEVDAAFPLERPDWDYTTQRGRNHLVLYRQ
LLLAGLQNAGRSPTNLAKVKGITQGPDESPSAFLERLKEAYRRYTPYDPEDPGQETNV
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KGHWAKDCPKKPRGPRGPRPQTSLLTLDD"
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Location/Qualifiers
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GGNGQLQYWPFSSSDLYNWKNNNPSFSBDPGKLTALIESVLTTHQPTWDDCQQLLGTL
LTGEEKQRVLLEARKAVRGNDGRPTQLPNEVDAAFPLERPDWDYTTQRGRNHIVLXRQ
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KGHWAKDCPKKPRGPRFREMSKLLATVYSGGRQDRQGGERRRPGLDKDQCAYCKE
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Pred. No. 0;
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayafatu, N., Hiranch, T., Hiraoka, T., Hiraoka, T., Hayafatu, N., Hiranch, T., Hiraoka, T., Hayafatu, M., Hayafatu, M., Hiraoka, T., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kohiaa, T., Miyazaki, M., Muraa, M., Ohaato, M., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Fakahashi, T., Takaku-Akahira, S., Takada, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission Hayashizaki, Y. Direct Submission Research (RIKEN) 'Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, I-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9226, Fax:81-45-503-9216, Tarsiya was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group, RIKEN Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \(\frac{\codon \text{start=1}}{\codon \text{start=1}}\)
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//organism="mana"

/strain="C3H"

/db_xref="FaNYTOM_DB:G431002F22"

/db_xref="faxon:10090"

/clone="G431002F22"

/cell_line="CRL-1443 BC3H1"

/cissue_type="brain"

/clone_lib="RIKEN full-length enriched mouse_cDNA_library"

629. _2242
    Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Samamoto, R., Matsuneto, H., Sakagurchi, S., Itsegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 8268)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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982 984

818 862 878 922

6.85 GAACHTCTTCTCAAAACCTCTATACAAACTTCTCTTTTTTCTAACTTCTT	RESULT 3 AKO90126 AKO90126 LOCUS DEFINITION MUS musculus brain CRL-1443 BC3H1 cDNA, RIKEN full-length enriched library, clone:G431002E14 product:gene el protein, full insert sequence. ACCESSION AKO90126 VERSION AKO90126.1 GI:26105743 KEYWORDS HTC; CAP trapper. SOURCE Mus musculus (house mouse)
5768 CCRTACTCROANTAGCCTCTOAACCCTCTAAAACCGCATACCGCTGGGCC 5827 5713 CCTTACTCROAATACCCTCTCAAACCCTCTCAAACCCGCTAGCACAGCCCG 5885 5920 CCCTACTCCTCTAATACCTCTCAAACCCTCTCAAACCCGCTTGGCAAACGCTGCAGC 5885 5920 CCCTACACCCTCTAATACCTCTCAAACCCTCTCAACCCGCTTGGCAAACCGTGTGGC 5885 5921 TATTAATACCTTTTTAACCTCTCAAGCACTACTAACCCTCTAACCCGAAACCGTGTGGC 5825 5922 TATTAATACCTTATTAACCTCTCTCAGCAACCTCTAACCCGAAACCGTGTGGC 5825 5924 CACCACGCTTTTTAACCTCTCTCTCAGCAACCTCTCAACCCCGAAACCGTGTGGC 5825 5924 ATTACCACACCTCTCTCAGCACTCTCTCACCCCCCAAACCGTGTGCC 5825 6006 GTTGGCCCTCCACACCCCTCTTTAATACTCTCACCCCCACAAACCGTGTGCCC 6055 5824 ATTACCGCAATCACCCCTCTTTAATACTTTGGCCACAAACCGTGAACCGTGTGTGC 6055 5825 ATTACCGCCAATCACCCCTCTTTAATACTTGGCCCCCCAAATACCGTGTACCTCTTAATACTTTTCTCTCACCCCCCAAATACCGTGTGCCCCCAAATACCGTGTGCCCCTAATACCGTTTAACTTTTTCTCTCACCCCCAAATACCGTGTGCCCCCAAATACCGTGTGCCCCTAATACCGTTTAACTTTTTCTCTAACTTAACTTTTTCTTTTTTTT	6478 ATCCAGGGGGTTTTCAAGCTCTTAACTCCACGAGTCCTCGGGGGTACCTTCTTGTTGG 6537  6726 GTAAAAGGAGCCTACCAACCTCACCACTCTGTTAAAAACCAGGGTGCTGG 6785  6538 CTATGCTTAGCTTCGGGCCCACCTTACTATGAAGGAATGGCTAGAAATCAAT 6597  6786 TTATGCTTAGTTCGGGCCCACCTTACTATGAAGGGGTTCCCTAGATACCTACTC 6845  6598 GTGACAAAAGAACAATGCAATGCACTACTACTACTACTACTACTACTACTACTACTACTACT

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                                                                                                                               /tissue_type="brain"
/clone lib="RIKEN full-length enriched mouse cDNA library"
1. 9283
/note="gene el protein (PIR|S48861, evidence: FASTY,
99.9%ID, 100%length, match=3565)"
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                                                                                                                                                                                                                                                                                                                                                                                Score 1679.6; DB 4; Length 8283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 2929;
/db_xref="FANTOM_DB:G431002E14"
/db_xref="taxon:10090"
/db_choe="d431002E14"
/cell_line="CRL-1443_BC3H1"
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55.5%;
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                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahikayi,K., Yonacaki,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer [Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 8283)
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                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site for further details.
URL:http://gnone.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                          Calinal, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/mol_type="mRNA"
/strain="C3H"
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1418 CTCACCACCCACCACCACCACCACAGANGATATATAGAGAAACTTACC   1477     1419 ACCCAGGACACACACACACACACACACAAAAAACTTACCCCGGACCACACGG   1439     1419 GAGCAACACACACACACACACACACACACACACACACAC	2189 TGCCCAAAGAACCAAGGACCCAAGGACCCCAGACCTCCTCCTCCTGACTTA 2248  2181 AAAGATTAGGGAGACCAGGGACCCCCAGACCTCCTCCTCCTCCTGACTTTA 2248  2181 AAAGATTAGGGAGACCAGGGCTCCGGAGACCCCCCAGCCTACCTCCTCCTGACTTTA 2248  2211 GAGGGCAACCAGTGAGTCCTGGTTGATACCGGAGAACATTCAGTGCTACTGC 2308  2211 GAGGGCAACCAGTTAGAGTTCCTGGTTGATACCGGAGAACATTCAGTGCTACTAGCT 2308  2211 GAGGGCAACCAGTTAAAAGATTAAAAAATTCTGGGTGCTACTGCTGCTACTAG 2310  2209 GGGGGCAACCCGTCACTTCTGGTTGATACTGGGTGCTCACTGGTGCTACTAGATACTGGTGCTACTGGTGCTACTAGATACTAGATAAAAATTAGATAAAAATTAGATAAAAATTAGATAAAAATTAGATAAAAAA

5481 5423 5003 5301 5421 AACGGGCTGCCTTCACCTCCCAGGTAAGTCAGTCGGTGGCCGATTTACTGGGGATCGAT TATGAATTACTCTACGGGGGCCCCCCCCATTGGTAGAAATTGCTTCTGTACATAGTGCT CACCCCTTCGGGATTGGAGACTCCGTGTGGGTGCGCCGGCACCAGAACTTAGAA 5655 TCGGGGTGGAAAGCCGAAAAGACTGAAAATCCCCTTAAGCTTCGCCTCCATCGCGTGGTT CCCCACAAAGAAGGGTTAGAATATGTCCAACAGATACATCGTCTAAACCCACCTAGGAACT 1822 cacaaaaricaaacacriccrigacagagagagagagagccccracracargcraaac GGAGTGGCTGGTGGTCAAACATTGTGTGCCCTGCCAGCTGGTTAATGCTAATCCT AATGGTCCAGCTTTTGTTGCCCAGGTAAGTCAGGGACTGGCCAAGATATTGGGGATTGAT TOGAAACTGCATTGTGCATACAGACCCCAAAGCTCAGGACAGGTAGAGGATGAATAGA 5242 riggaaarracarrigrigcriraragaccccagagrircaggricaggragaaagaargaaraga ACCATTAAAGAGACCCTTACTAAATTGACCGCGGAGACTGGCGTTAATGATTGGATAGCT CTCCTGCCCTTTGTGCTTTTTAGGGTTAGGAACACCCCTGGACAGTTTGGGGCTGACCCCC CTACTCCCCTTAGCTCTCTACCGAGCCCGGAACACTCCGGGGCCCCCATGGATTGACTCCG 5422 TATGAAATCTTGTACGGGGGCGCCCCCTTGTCAACTTCCATGACCCCGAAGTGTCA gaartaactaatagcccarctcccaagctcacrtacaggccctccaaacggtgcagcga CGAGCGTGGAGGCAACTCCGGGAGGCCTACTCAGGAGGAGGAGGAGTTGC---AGATCCCA CATCGTTTCCAAGTGGGAGATTCAGTCTACGTTAGACGCCACCGTGCAGGAAACCTCGAG GGAATCTCCACCTGGATCCATGCATCCCACGTTAAACCGGCGCCACCTCCC----GAT GGCATCTCTGCATGGATACACGCCGCCACACGTCAAGGCAGCGACCACACCCCGATAAAA AAACACCTGCAGCAGTTGGTCA-----GAACATCCCCTTATCATGTTCTGAGGCTACCA AAAACCCTCCAATATGTGGCAGATTCCTGCACGTCTGTGCCCAAGTAAATGCCAGAAA TCCAGAATGCCTCCAGGGAAGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTG GACTTCACTGAGGTAAAGCCGGCTAAATACGGAAACAAATACCTATTGGTTTTTGTAGAC GATITIACAGAAGTCAAGGCCAGAGCTATATGGGTACAAGTACCTCCTGGTATTCGTGGAC ACCITITICAGGAIGGGIAGAGGCITATCCIACTAAGAAAGAGACITCAACCGIGGIGGCI acciricitorio de la contración de la con 5182 5304 5424 5541 4824 4942 4884 5002 4944 5062 5004 5122 5064 5124 5184 5244 5362 5364 5482 5481 5602 5601

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Qy         6654 TACTGAGGTTTCTGGAAAAGCCACCTGCATAGGAAAGGTTCCCCCATCCCAACACCT         6713           bb         6917 GTCCGAAGTGACCAGGAACTCTCGCATAGAGCGGTCCCTAAAACCCATCAAGTCTT         6976           Qy         6714 TTGTAACCACACTGAAGCCTTTAATCAAACCTCTGAGGAGTACTGGTACCTGGTTACTGGTACCTGGTTACCACCTTGGTACTGGTACCTGGTACTATTTTAGGCCGCTCCCAC         7030           Db         6977 GTGTAATACCACCCAAAAGACAAGCGATGAATAACCCCTTGGTTTTCGCCGCTCCCAC         7030           Qy         6774 TGACAGGTGGGGGGTGTAATACTGGATTAACCCCTTGTGTTTTTAA         6833           Db         7031 AGGAACTACCTGGACTACTCGCATCTCAACCACCACTTGTTTTAA         6833	6834 CCAAACTAAAGATTTTTGCATTATGGTCCAAATTGTTCCCCGAGTGTATTACTATCCCGA	7208	Oy 7062 ACATCGAATTGTAACAGAGATCTCCAACACTGTAACAGAAATCTGTAGTAACATCTGTAACACAAAA 7372  Db 7313 CCAGGCTGCCATGCACGATGACCTTAAAGAAGTTGAAAAGTCCATCACTAATCTAGAAA 7372  Oy 7122 ATCCCTAACCTCATATCTGAAGTAGTCCTACAGAATAGAAGAGGCTTAGATTATTATT 7181  Db 7373 ATCTTTGACCTCTTGTCCGAAGTAGTGTTACAGAATCGTAGAGCCTAGATCTACTATT 7432  Oy 7182 TCTAAAAGAAGGAGGATTATGTGTGTAGCCTTGAAGGAGGATTTTATGTGGATCA 7241	7433 C 7242 T 7493 C 7302 G	QY         7362 TACCCTACTITCGCTTTAACAGGACCCTTAATAGTCCTCCTGCTTACTCACAGTTGG         721           Db         7613 CACCTGATATCCACCATCATGGGTCCCTGATAATTTTACTCTTTGG         7672           QY         7422 GCCATGTATTATTAACAAGTTAATTGCCTTCATTAGAGAACGAATAAGTGCAGTCCAGT         7481           Db         7673 GCCTTGTATTATTATCAATGCCTTCATTAGCAAGACAGGATTTCGGTAGTGCAGGC         7732           QY         7482 CATGGTATTTAGACAACAGTACCA         7505           Db         7733 CCTGGTTCTTAGACAACACAATATCA         756           Db         7733 CCTGGTTCTTAGACAATATCA         756	RESULT 4 AK090125 LOCUS AK090125 LOCUS DEFINITION Mus musculus brain CRL-1443 BC3H1 cDNA, RIKEN full-length enriched library, clone:G431002D05 product:gene el protein, full insert sequence. ACCESSION AK090125.1 GI:26354958 KEYWORDS HTC; CAP trapper. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus
	Db 5960 AATAACCGGCAATCACCCTCTGTGGACTTGGTGGCCTCACCACCACATCTCTG 6016  QY 5879TATACGTTTGCCTCAGATCAGTTATTCCTAGTCTGACC 5916  Db 6017 TATGTTGGCCCTCCACGGCCGTCCTATTGGGGCTTAGAATATCGGGCTCCTTTTTCTCC 6076  QY 5917 TCACCC	5930 6137 5990 6197		AACTC 64 AACTC 64 AATGG 62 CATTG 64 CGCCT 63	Db 6497 GTGGGGÄTTGCGCCTATACGTCTCTGGACATGÄCCCÄĞGGCTCATCTTGGGATCCGACT 6556  Qy 6312 CAAATAAACCAGCTGGAGCCTCCAATGGCCAAATACGGTCTTGACGGCTC 6371	OY 6474 CCTCATCCAGGAGCTTTTCAAGCTCCACGACTCCAGGAGGCTACCTCTTTG 6533

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/ LTAIN 1 AL 10H - "MOGTVTTPLSLTLEHWEDVQRIASNQSVDVKKRRWVTFCSAEWP
TFGVGWPQDGTFNLDIILQVKSKVFSPEGPHGHPDQVPYIVTWEAIAYEPPWKKPFVS
PRASPSPFAFILBSGBSTQPPPRSALYPSIKRPRSKPGVUSDNGGPLIDLLSED
PPYGGQGPSSSDGDREEATSTESIPAPSPP1KRPRSKPGVUSDNGGPLIDLLSED
PPYGGQGPSSSDGDREEATSTESIPAPSPP1KRPRSKPDPPADSTTSRAFPLRL
GGNGQLQYWPFSSSDLYNWKNNNPSFSEDPGKLTALIESVLTTHQPTWDDCQQLLGTL
LTGEEKQRVLLEARKAVRGNDGRATQLPNEVDAAFPLERDWDYTTQRGRNHIVLYRQ
LLAGAGLOMAGRSPTULAKVRGTTQGDBSPSAFLERLKEAYRRYTPYDPEDPGQETNV
SMSFYWGSAPDIGRKLERLEDLKSKTLGDLVKSKTLGDLVKBAERIFTRERKEYFRFETER
EERRRAEEEQKRKERDRRRHREMSKLLATVVSGQRQDRQGGERRRPQLDKDQCAYCKE
KGHWAKDCPKKRPRGPRGPRPQTSLLTLDD"
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                                                                      tissue_type="brain"
Colone_lib="RIKEN full-length enriched mouse cDNA library"
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'note="unnamed protein product; gene el protein
(PIR|548861, evidence: FASTY, 99.9%ID, 100%length,
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Pred. No. 0;
0; Mismatches 2935; Indels 278;
                                              line="CRL-1443 BC3H1"
                                                                                                                                                                                                                                   codon_start=1
/proteIn_id="BAC41106.1"
/db_xref="G1:26354959"
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/note="putative"
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Best Local Similarity 55.5%;
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                                                                                                                                                                                                                                                                                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonake,S., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 11076861
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Chordata, Craniata, Vertebrata, Buteleostomi,
Buarchontoglires; Glires; Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
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/strain="C3H"
/db_xref="FANTOM_DB:G431002D05"
                                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
    Eukaryota; Metazoa; Chordata; Cranis
Mammalia; Eutheria; Euarchontoglires
Sciurognathi; Muridae; Murinae; Mus.
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URL:http://fantom.gsc.riken.jp/
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1311 GAGGGCTGGGGGGTCGGGGGCCCCCTGAACCCGGGAACACCCCCCCC
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10195 GAGGGACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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/mol type="mRNN"
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/cell line="CRL-1751 WEHI 164"
/clone lib="RIKEN full-length enriched mouse cDNA library"
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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99.9%ID, 100%length, match=3565)"
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Please visit our web site for further details.
Please visit our web site for further details.
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/_organism="mus musculus"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Let (10,700 full-length CDNAs

Let
                    10739 TIGIATICTCAATCGCCTGGTCCAGTTTATCAAAGACAGGATTTCGGTAGTGCAGGCCCT 10798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramstsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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Ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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221 GAGGGGCAACCAGTTGACTTCAGTTGATACCGGAACACATTCAGTCCACTCAGTCACTCAGTCAG
6 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4
1116 GAMGAGCCACCTCCACTTCTGCACTTCTCCCCCTTCTCCCATAGTTCTCCCCCTCCCCTTCTCTCCCCTTCCCCTTCTCCCCTTCTC

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5823 TATTAATAICAACAACACTCAAGG
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7312 AGAAGAGGTTAGATTTATTTTT 7184 GAATGCTGTTTTATGTGGATCATTC 7244 7304 TTCAACAGGTCTTTTGGTTGGCTAC 7364 7424 Crcrrgrraarrracrcrrrgggcc 7672 GAACGAATAAGTGCAGTCCAGATCAT 7484 6836 6956 7207 7267 CTAGAAACAGGACTTAGTAACCTACA 7064 AAATCTGTCAGTAACCTGGAGGAATC 7124 dalakartidagtcakakakakakar 7552 SGATCCCAAAATAAGCTTACCCTTAC 6656 STRECCCCATCCACCACACCTTG 6716 AGTCAATATCTGGTACCTGGTTATGA 6776 CTTGGAGTGGCAGGTGTAGGAAC 7004 6736 6536 9619 rccracrarrrdccccrccacade 7030 CCCGAGTGTATTACTATCCCGAAAA 6896 SGAATGGCTAGAAGAGGGAAATTCAA 6596 GAAAGGTTGGAGAAGCGTCGAAGGGA CICCICCIGITACICACAGITGGGCC rgrgrtrccaccrrggrtrtraacca GCCGCAATTGCCGCTGGAGTGGGAAC 3GAGTCGAAACCGATTGTTAAATCT ACTCCAGAGGCTACCTCTTCTTGTTG Greergaraaacecaagagreerg caacaa----crcca AAATGGGGGCAAAACTTTTAGCCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="retina"
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/dev_stage="adult"
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Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers
                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATGGCCTCTCCCCTTTACCTCCTCATATCCCCAACCCCAATTATCCGCTCCTCCCCTC
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                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A930033E24"
/db_xref="taxon:10090"
/clone="A930033E24"
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Pred. No. 0;
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Best Local Similarity 63.0%;
Matches 2392; Conservative
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Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Haramoto, K., Hirozane, T., Hayashida, K., Hayateu, N., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, A., Ohno, M., Ohsato, N., Okazaki, Y., Satch, R., Saitch, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                              AXO44688

Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930033E24 product:unclassifiable, full insert sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Functional annotation of a full-length mouse cDNA collection
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4147)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                 GGTTCTGACTCAACAATATCA 7753
                                                                                                                                                                                                                                                                                                               HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Chordata, Craniata, Vertebrata, Euteleostomi,
Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Reele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                              Contact: Smith TPU
Contact: Smith TPU
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified w
cross match v0.990329.
Plate: TMW8027 row: F column: 1
Seq primer: TAGAAGCAAGCAAGG.
Location/Qualifiers
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/db xref="taxon:9823"
/tissue_type="pooled"
/lab host="FH108"
/clone_lib="WARC 4F1G"
/note="Vector: poDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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Best Local Similarity 98.5%; Pred. No. 5.4e-223;
Matches 833; Conservative 0; Mismatches 13;
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EST 12-JAN-2004

CK455881 848 bp mRNA linear 916502 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.

2564

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2504

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**Gaps** 

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Pred. No. 6e-217; 0; Mismatches 20; Indels

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360

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480

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TCAGTCAGACAGTACCCCTTGAGTAAAGAAGCTCGAGAAGGAATTCGGCCGCCATGTTCAA
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                                                                                                                                                                                   CCATTAGGAAAACTAAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAACAG
                                                                                                                                                                                                                                                                                                    241 CCATTAGGAAAACTAAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAAAA
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                                          GGCAATAGGACCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAAAAAGGACACTGG
                                                                                                     2091 GCAAGGAACTGCCCCAAGAAGGAAACAAAGGACCAAGGATCCTAGCTCTAGAAGAAGAT
                                                                                                                         2151 AAAGATTAGGGGAGACGGCGTTCGGACCCCCTCCCGGGGCCCAGGGTAACTTTGAAGGTG
                                                                                                                                                                                                                         GAGGGGCAACCAGTTGAGTTCCTGGTTGATACCGGAGCGAAACATTCAGTGCTACTACAG
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97.68;
   Best Local Similarity 97.6
Matches 816; Conservative
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Sus scrofa
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Nonmean, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fex: 402 762 4356
Fex: 402 762 4350
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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                    GGGATGGGTTTGGCAAAGCAAGTTCCCCCACAAGTTATTCAACTGAAGGCCAGTGCCACA 2684
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/organism="Sus scrofa"
/mol type="mRNA"
/db xref="mRNA"
/tissue type="pooled"
/lab host="DH10B"
/clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                       69
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                                                                                                                                    GTCAATAAACGGGGGGGGGATATACACCCCAACAGTCCCCGAACCCTTATAACCTCTTGTGT
                                                                                                                                                                                                                                                                         128 GTCAATAAACGGGTGCAGGATATACACCCAACAGTCCCGAACCCTTATAACCTCTTGTGT
                                                                                                                                                                                                                                                                                                                                   68 GCTCTCCCCACCCCAACGGAGCTGGTATACAGTATTGGACTTAAAGGATGCCTTCTCTCTGC
                                     368 GGGATGGGTTTGGCAAAGCAAGTTCCCCCACAGGTTATTCAACTGAAGGCCAGTGCTGCA
                                                                              CCAGTGTCAGTCAGACAGTACCCCTTGAGTAAAGAAGCTCAAGAAGGAATTCGGCCGCAT
                                                                                               308 CCAGTGTCAGTCAGACAGTACCCCTTGAGTAAAGAAGCTCGAGAAGGAATTCGGCCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called wi
trimmed with the aid of the trim_alt op
cross match v0.990329.
Plate: TWW8027 row: F column: 1
Seq primer: GTAATACGACTCACTATAGGG.
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CK454836
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; EST 15-FEB-2005 DN124474 1125381 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence. DN124474 GI:59818753 EST. (bases 1 to 835) REFERENCE

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1840
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                                                                    1051 GTGCCGCGAGGGGACCCTTTGCCCCTCCTGGAGCTCCGGCGGTGGAGGGACCTGCTGCTGCAG 1110
                                                                                                                                          GGACTCGGAGCCGGAGCGCCCCCCGGAGCGGACAGACGAGATCGCGACATTACCGC 1170
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Nonneman, D.J., Wray, J.E. and Keele, J.W.
Nortine B.D. Str collection using a normalized library constructed from embryos representing early developmental stages
Unpublished (2003)
                                 184
                                                                                                                                                                              64
                                                                                                                                                                                                                 TGCGCACGTACGGCCCTCCCACACCGGGGGCCAATTGCAGCCCCTCCAGTATTGGCC 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified w
cross match v0.990329. Column: 19
Plate: HHY8024 row. O column: 19
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                        aagggagacagaagaaaagggaacaaagaaaaagagaaagaaaggaagga
 AGGAGCCACCGGCTTGGCCGGAACCCCAATCTGTTCCCCCCACCCCCTTATCTGGCACAGG
                  243 AGGAGCCGCCGGCTTGGCCGGAACCCCAATCTGTTCCCCCAACCCCTTATCCGGCACGGG
                                                                                                                                                               9
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/db xref="taxon:9823"
/tishust="phooled"
/lab host="DH10B"
/clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibxery made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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1122855 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
DN122618.1 GI:59816897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
9.4%; Score 761; DB 8; I
Best Local Similarity 97.5%; Pred. No. 1.1e-204;
Matches 773; Conservative 0; Mismatches 20;
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/organism="Sus scrofa"
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Sus scrofa
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Norcine EST collection using a normalized library constructed from embryos representing early developmental stages Unpublished (2003)
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                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
cross_match v0.990329.
Plate: HHY8028 row. H column: 24
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
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/db_tref="texnoss"
/lab_host="DH108"
/clone lib="WARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoR1; Site_2: Not1; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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Pred. No. 1e-208;
0; Mismatches 23; Indels 8
                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4366
Fax: 402 762 4399
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CEST The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harab, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoco, K., Hiraoka, T., Hirozane, T., Hayashida, K., Mayasaki, T., Mayasa, I., Kasukawa, T., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kaswai, T., Katoh, H., Kawai, J., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Saroo, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tanaka, T., Towaru, A., Toya, T., Yasunishi, R., Sakazume, N., Saitoh, H., Sakazume, N., Saitoh, H., Sakazume, Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Takaku-Akahira, S., Takaku-Akahira, S., Sano, H., Shaganizaki, Y., Saitoh, Muramatau, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A., Kohama institute of Group, RIKEN Genomic Sciences Center (GSC), RIKEN Genome Conton Ruchttp://genome.gsc.riken.jp/, Tel:81-65-503-9222, URL:http://genome.gsc.riken.jp/, Tel:81-65-503-9222, CNN All Sprace Conton Conton Ruchttp://genome.gsc.riken.jp/, Tel:81-65-503-9222, CNN All Sprace Conton Conton
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
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/clone lib="RIKEN full-length enriched mouse cDNA library"
               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunco,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase II Team and the

    .3442
/note="murine repeated virus, Y linked (MGD|MGI:97238,
GB|X87639, evidence: BLASTN, 96*, match=1678)"

                                                                                                                                                                                                                                                                                                                                                                                                                     FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Pred. No. 2.5e-201;
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/db_xref="taxon:I0090"
/clone="F730005P06"
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/strain="C57BL/6J"
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Mus musculus B6-derived CD11 +ve dendritic cells CDNA, RIKEN full-length enriched library, clone:F730005P06 product:murine repeated virus, Y linked, full insert sequence.
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AAGACGTAATAAACGGCAAGAGAAGTTTGACTAAGATCTTGGCTGCAGTGGTTGAAGG 614
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AK089325.1 GI:26105207
HTC: CAP trapper.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                     133 CAAGATGGGAGCACAAATTTTTTTTTTTGAACAAGGAAAACCAGAAGTGTCTGCAAATAACAA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                             /cell_type="fibroblast"
/clone_lib="SBAB"
/note="Genoscope sequence ID : IH0AAA30CE08RM1"
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Pred. No. 5.8e-201;
0; Mismatches 30;
BP 191 91006 EVRY cedex - FRANCE (B.

- Web : www.genoscope.cns.fr)
Location/Qualifiers
i. . 797
/ organism="Sus scrofa"
/ fstrain="Large White"
/ db xref="Laxon:9823"
/ clone="bl0295H10"
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Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage
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                                                      TGGGTTTGGCAAAGCAAGTTCCCCCACAAGTTATTCAACTGAAGGCCAGTGCCACAC
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Rogel-Gallard, C., Bourgeaux, N., Billault, A., Vaiman, M. and
Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chardon, P., Iannuccelli, N., Roig, A., Dossat, C., Demars, J., Rogel-Gaillard, C., Roy, A., Schibler, L. and Milan, D. A physical map of the swine genome Unpublished
3 (bases 1 to 797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Construction of a swine BAC library: application to the characterization and mapping of porcine type C endoviral Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
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GSS; Bac-end sequence BES; Genome Survey Sequence
Sus scrofa (pig)
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Mammalia; Eutheria;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4350
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
plate: TWW8053 row: M column: 24
Seq primer: TAGAAGGCAAGTCGAGG.
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                         361 CCGGAAGGAACTTCAGCACAAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTGCGGCTG
                                                                                                                                                                                                     GTACATGGGGCCATCTATAAACAAAGGGGGTTGCTTACCTCAGCAGGAGGGAATAAAG
                                                                                                                                                                                                                                                            601 ATACACTGTCCTGGACATCAGAAGCTAAAGATCTCATATCCAGAGGAAACCAGATGGCT
CCGGAAGGAACTTCAGCACAAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTGCGGCTG
                                                                                       4230 GCCGAAGGGAAATCCATAAACATTTATACGGACAGCAGGTATGCCTTTTGCGACTGCACAC
                                                                                                           GCCGAAGGAAATCCATAAACATTATACGGACAGCAGGTATGCCTTTGCGACTGCACC
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/lab_host="DH10B"
/clone_lib="MARC_4PIG"
/clone="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not1
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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Pred. No. 5.9e-196;
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Sus scrofa
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Best Local Similarity
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CN159699/c
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Plate: TWW8053 row: M column: 24
Seq primer: GTAATACGACTCACTATAGGG.
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
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Porchae EST collection using a normalized library constructed from embryos representing early developmental stages
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fel: 402 762 4386
Feax: 402 762 4380
Email: smith@email.marc.usda.gov,
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/mol type="mRNA"
/db_xref="texan:9823"
/tissus type="pooled"
/lab_host="DH108"
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/note="Vector: pcDNA3.1; Site_1: EcoR1; Site_2: Not Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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9.0%; Score 730.4; DB 7; Length 733;
Best Local Similarity 99.9%; Pred. No. 5.9e-196;
Matches 731; Conservative 0; Mismatches 1; Indels 0
                                                                                                              CN157762 733 bp mRNA linear 946489 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence. CN157762
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    GGCCCTCACACAAGCT
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Sus scrofa
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CN157762
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fax: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
Plate: HHY8029 row: C column: 1
Seq primer: TAGAAGGCACAGTGAGG.
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                                                                                                                                                                        /organism="Sus scrofa"
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/db_xref="taxon:9823"
/tissue type="pooled"
/lab_hogt="DH10B"
/clone lib="WARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibxary made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
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Pred. No. 1.6e-193;
0; Mismatches 65; Indels
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Best Local Similarity 91.1%;
Matches 793; Conservative
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Sumamalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Nonchan,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
Unpublished (2003)
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QQ	150	150 ACAGCACTCAAGGGAGGCTCCCTTGGGGACCTGATGGCCTGAATTATATATGTCTGCCTTC 91
δ	5894	5894 GATCAGTTATTCCTAGTCTGACCTCACCCCAGATATCCTCCATGCTCACG 5944
q	90	90 GATCAGTAATCCCTGGTCTCAATGACCAGGCCACACCCCCCGATGTACTCCATGCTTACG 31
ò	5945	5945 GATTTTATGTCCCAGGACCACCAAATA 5974
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Search Job tim	complete : 19;	Search completed: February 5, 2006, 05:13:18 Job time : 19203 secs

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Sequence 18,

Sequence

Sequence Sequence Sequence

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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Sequence 3, Application/US/08766528

Patent No. 6190861

GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STREET: MASACHUSELTS
COUNTRY: USA
COUNTRY: USA
TIP: 02109-1875
COMPUTER: MEDIUM TYPE: Floppy disk
COMPUTER: MEDIUM TYPE: Floppy disk
COMPUTER: TIEM PC Compatible
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/766,528
FILING DATE:
PRIOR APPLICATION NUMBER: US 08/572,645
FILING DATE:

PRIOR APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: MGP-038CP
TELEFRANCE/DOCKET NUMBER: MGP-038CP
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US-09-718-08-11
US-09-111-085-1
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US-08-111-085-1
US-08-111-085-1
US-08-111-085-1
US-08-011-745-3
US-09-011-745-4
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US-09-171-553B-9
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US-09-25-013-3
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 8132; Conservative
                                          STRANDEDNESS: single
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; MOLECULE TYPE: CDNA
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1640.2
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                            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2 6/ptodata/1/ina/5_COMB.seq:*
/cgn2 6/ptodata/1/ina/6_COMB.seq:*
/cgn2 6/ptodata/1/ina/RE_COMB.seq:*
/cgn2 6/ptodata/1/ina/RE_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
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/cgn2 6/ptodata/1/ina/PE_COMB.seq:*
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US-09-171-553B-2

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US-08-766-528-2

US-09-661-858-2

US-09-661-858-2

US-09-661-858-2

US-09-661-858-2

US-09-171-553B-1

US-09-171-573B-1

US-09-315-127-4

US-09-315-127-4

US-09-315-127-4

US-09-315-127-4

US-09-315-127-4

US-09-315-127-4

US-09-315-318-3

US-09-316-358-420-13

US-09-316-388-642-8

US-09-433-322B-2

US-09-433-322B-2

US-09-376-781-25

US-09-376-781-25

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Score

Result

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Length 8132; Indels

8040

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AAAACTGGTTGCGCCATAAAGATGTTGAAATGTTGATACACATATCTTGGTGACAACATG
                                                                                                                  CCACGAAGCGCGGGCTCTCGAAGTTTJAAATTGACTGGTTTGTGATATTTTGAAATGATT
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                                                                                                                                                                                                                                                              GGTTTGTAAAGGGGGGCTTTGTTGTAGAACCCCATAAAAGCTGTCCCGACTCCACTCG
                                                       TCTTGAAACTATTTGAGATAACAAGAAAAGGGAGTTTCTAACTGCTTGTTTAGCTTCTGT
                                                                     TCTTGAAACTATTTGAGATAACAAGAAAAGGAGTTTCTAACTGCTTGTTTAGCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/661,858
FILING DATE: 14-Sep-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,528
FILING DATE: «UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8112 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09661858
Patent No. 6699663
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COC
STREET: 60 State Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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US-09-661-858-3
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TGCTTAGCTTCGGGCCCACCTTACTATGAAGGAATGGCTAGAAGAGGGAAATTCAATGTG 6600
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                      CACACTGAAGCCTTTAATCAAACCTCTGAGAGTCAATATCTGGTACCTGGTTATGACAGG
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	7958 8007 8067 8063 8127 8123 8123	RESULT 4 US-09-171-553B-2  Sequence 2, Application US/09171553B  Patent No. 6756227  GENERAL INFORMATION:  APPLICANT: GALBRAITH, DANIEL N.  APPLICANT: HAWORTH, CHRISTINE  APPLICANT: LEES, GILLIAN M.  TITLE OF INVENTION: POMCINE RETROVIRUS  FILE REFERENCE: CFV-5.01  CURRENT FILING DATE: 1999-02-08  PRIOR APPLICATION NUMBER: PCT/GB97/01087  PRIOR APPLICATION NUMBER: GB 9702668.6  PRIOR APPLICATION NUMBER: GB 9702668.6  PRIOR PILING DATE: 1997-04-18  PRIOR FILING DATE: 1997-04-19  NUMBER OF SEQ ID NOS: 17  SOFTWARE PATENT NUMBER: GB 9608164.1  PRIOR FILING DATE: 1996-04-19  NUMBER OF SEQ ID NOS: 17  SEQ ID NO 2  LENGTH: 8196  TYPE: DNA  TYPE: DNA  CREANISM: POLCINE FELTOVÍTUS
6416 CTGGATCAGACCCCACTGAGTCTAACAGCACGACTAAAATGGGGG 6460 6452 CTGGATTGATTCCTACCAACACGCCTAGAAACTCCCCCAGGTGTTCCTGTTAAGACAGGAC 6511 6461 CAAAACTTTTAGCCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACGACG 6520 6512 AGAACTTTTTAGCCTCATCCAGGAGCTTTTCAAGCCATCACTCCACGACG 6571 6521 CTACCTCTTCTTGTTGGCTATGCTTAGGGCCACCTTAACTATGAAGGAATGGCTA 6531 6522 CTACCTTCTTCTTGTTGGCTATGCTTAGGGCCCACCTTAACTATGAAGGAATGGCTA 6531 6532 AGAAGACATTCAATGTCAAAAGACTTCCAGGGCCACCTTAATATGAAGGAATGCCAA 6631 6533 AAAAGCTTACTCTTGTTGTTATTCAAAAAAAAAAAAAAA	6812 CCTCAGTCTTCAACCAATCCTAAAATTTCTCTGTCCAATCCAAATCGTCCCCCCGAGTGT 6931 6881 ATTACTATCCCGAAAAAGATTTCTGTGTCTACAAAACAACAAAGA 6940 6932 ACTACCATCCCGAAAAGCAATCCTTGATGAATAACACAAAACAAAGAACAACCAAC	121   AATCCCTAACCTCCTTATCTGAAGTAGTCCTACAGAATAGAAGAGGGTTAGATTATTAT   180

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 5521; Conservative 0; Mismatches
REGISTRATION NUMBER: 35,965
REFERENCE/OOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 8060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: MOLECULE TYPE: CDNA
US-08-766-528-1
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Oy         5459 AGGAGGAGTTTGCAGATCCCACATGGTTTCCAGGTGGGAGATTCAGTCTAGGACG         5518           Db         7985 AGGAGGAGTTTGCAGATCCCACATCGTTTCCAAGTGGGAGATTCAGTCTAGGTTAGACG         8044           Oy         5519 CCACCGTGCAGGAAAC         5534           Db         8045 CCACCGTGCAGGAAAC         8060	RESULT 7 US-08-766-528-2 ; Sequence 2, Application US/08766528 ; Patent No. 6190861 ; Patent INFORMATION: ; APPLICANT: Jay A. Fishman ; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS	: AND METHODS OF USE S: 74 RES: COCKFIELD, LLP B Street	ZIP: 02109-1875  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA:	8/572	; ATTOKNEY AGENT INPORMATION: ; ATTOKNEY AGENT INPORMATION: ; REGISTRATION NUMBER: 35,965 ; REFERENCE/DOCKET NUMBER: MGP-038CP	IELECOMONICIENTON INFORMATION:     TELEPHONE: (617)227-7400   INFORMATION FOR SEQ ID NO: 2:   CONTINUE CHARACTERISTICS	STATE   TOTAL STATE	A)	Query Match Best Local S Matches 6531	5 - 5 - 5 - 5 - 5 - 5 - 5			172 TAACACCGAGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAGGTGTATGCATGTA 	Dy 232 CCGGCCGGCGTCTCTGTTCTGAGTGTCTGTTTTCAGTGCGCGCTTTCGGTTTCGGTTTCGGC 291
Qy         4380 GCCGTACATTTACCAAAAAGGCTAGCTATTATACACTGTCCTGGACATCAGAAAGCTAAA 4439           Db         6906 GCCGTACATTTACCAAAAAGGCTAGCTATTATACACTGTCCTGGACATCAGAAAGCTAAA 6965           Qy         4440 GATCTCATATCCAGAGGAAACCAGATGGCTGACCGGGTTGCCAAGGCAGGC	4500 7026 4560	4620 TGCTATACCTCAGATGGGAAGCAATCCTGCCCCCACAAGAAGGGTTAGAATATGTCCAA  1145 TGCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAGAAGGGTTAGAATATGTCCAA  4680 C-AGATACATCGTCTAACCCACCTAGGAACTCAAAGAAGGGTTAGAATATGTCCAA  1680 C-AGATACATCGTCTAACCCACCTAGGAACTAAAAACACTGCAGAAGTTAGGTCAAGAACACTCAAAAAACACTGCAAGAACAACAACAACAACAACAACAACAACAACAACAA	4739 CCCTTATCATGTTCTGAGGCTACCAGGAGTGACTCGGTGGTCAAACATTGTGTGCCCCTAAACATTGTGTGCCCCCTATCATGTGTGTG		Oy 4919 CAPATROCTATTGGTTTTTGTAGACCCCTTTTCAGGATGGGTAGAGGCTTATCCTACTAA 4978	OY 4979 GAAAGAGACTTCAACCGTGGTGGCTAAAAAATACTGGAAGAATTTTCCAAGATTTGG 5038	OY 5039 AATACCTAAGGTAATAGGGTCAACAATGGTCCAGCTTTTGTTGCCCAGGTAAGTCAGGG 5098	Qy         5099 ACTGGCCAAGATATTGGGGATTGATTGGAAACTGCATTGTGCATACAGACCCCAAAGCTC 5158           Db         7625 ACTGGCCAAGATATTGGGGATTGATTGGAAACTGCATTGTGCATACAGACCCCAAAGCTC 7684	Oy         5159 AGGACAGGTAGAGGATGAATAGAACCATTAAAGAGACCCTTACTAAATTGACCGCGGA 5218           DD         7685 AGGACAGGTAGAAGGATGAATGAAACCATTAAAGAACCCTTACTAAATTGACCGCGGA 7744	Oy         5219         GACTGGCGTTAATGGATTGGATAGCTCTCCTGCCCTTTGTGCTTTTTAGGATTAGGAACAC         5278           DA         7745         CACTGGCGTTAATGATTGGATAGCTCTCTCTGCCCTTTTGTGCTTTTTAGGATTAGGAACAC         7804	5279 CCCTGGACAGTTTGGGCTGACCCCCTATGAATTACTCTACGGGGGACCCCCCCATTGGT	5339 AGAAATTGCTTCTGTACTGCTGACGCGTGCTTTCCCAGCCTTTGTTCTCTAGGCT  51319 AGAAATTGCTTCTGTACTAGTGCTGACGTGCTTTCCCAGCCTTTGTTCTCTAGGCT  51319 AGAAATTGCTTCTGTACTAGTGCTGAATGTGCTTTCCCAGCCTTTTGTTCTTCTAGGCTT  72655 AAAAATTGCTTCTTTATAGTGCTGAATGTGCTTATCCTTAGTCTTTCTT		

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		1445 CCGACGGCGACCCCCCAAATGAATTGACATTGACATTGCCTTGACTCGCC	TCATTGGGCAGTCCGGCTCTGGATATCAGGAAGAAACTTCAGAGAACTTCAGAAGGCTTACAGG AGGCTGGCACTCGGCTCTGGAAGAAACTTCAGAGAACTTCAGAAGGCTTACAGG AGGCTGGCTCTGGCTCTGGTGAAGGAAGGAAACTTCAGAGAACTTGCAGGAACAGGAACAGGAACAGAACAGAACAGAAACAGAAAGAACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAA
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                                                                                              CCTGCTGGCTGCCAGTAAATAGGTAGAAGGTCACACTTCCTATTGTTCCAGGGCCTGCTA
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APPLICANT: GALBRAITH, DANIEL N.
APPLICANT: GALBRAITH, DANIEL N.
APPLICANT: GALBRAITH, CHRISTINE
APPLICANT: BANGRH, CHRISTINE
APPLICANT: LEES, GILLIAN M.
APPLICANT: LEES, GILLIAN M.
APPLICANT: BANTH, KENNETH RETROVIRUS
FILE REFERENCE: CFV-5.01
CURRENT APPLICATION NUMBER: US/09/171,553B
CURRENT APPLICATION NUMBER: PCT/GB97/01087
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-10
PRIOR FILING DATE: 1997-04-10
PRIOR FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 17
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.8%; Score 2915.2; Best Local Similarity 94.3%; Pred. No. 0; Matches 3051; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Porcine retrovirus
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Pred. No. 0;
0; Mismatches 2575; Indels 285;
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                                                                                            APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TWO EMBARCAGES:
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STAME: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/075,272
FILING DATE: 08-MAY-1998
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILLING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 14538A-003710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Sequence 1, Application US/09075272 Patent No. 6136598 GENERAL INFORMATION:
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Matches 4377; Conserva
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Patent No. 6448390

GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY Of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127

CURRENT FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4
                                                                                                                                                            AGAAGCGTCGAAGGGAAAAGGAAACTACTCAAGGGTGGTTTGAGGGATGGTTCAACAGGT
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US-09-315-127-4
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US-09-315-127-4
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NAME/KEY: misc feature
; LOCATION: 1..8535
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                                                                                                      GCATTATGGTCCAAATTGTTCCCCGAGTGTATTACTATCCCGAAAAAGCAATCCTTGATG
                                                                                                                                                    cciaigacaaitcrcacccaagactaaaagagagccrgtcrcactraccraactarr
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ATAGAGACCAATGCACATGGGGATCCCAAAATAAGCTTACCCTTACTGAGGTTTCTGGAA
                                            CCTTTAATCAAACCTCTGAGAGTCAATATCTGGTACCTGGTTATGACAGGTGGTGGCATT
                                                                               TGCTCGGACTTGGAGTGGCAGCTGTAGGAACAGGAACAGCTGCCCTGGTCACGGGAC
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Sequence 3, Application US/09111085 Patent No. 6100034

RESULT 13 US-09-111-085-3

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Pred. No. 0;
0; Mismatches
GENERAL INFORMATION:
APPLICANT: Stoye, Jonathan P
APPLICANT: Wedse, Robin A
TITLE OF INVENTION: Detection of retroviral
TITLE OF INVENTION: Specific sequences
FILE REFERRNCE: 4238/75168
CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
BARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.0
                                               retroviral
                                                                                                                                                                                                                                                                                        Query Match 24.8%;
Best Local Similarity 76.3%;
Matches 2670; Conservative
                                                                                                                                                                                                                                             retrovirus
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Pred. No. 0;
0; Mismatches 2919;
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Similarity 56.0%;
56; Conservative
                                                                                                                                                                                                                                           genomic DNA
201-994-1700
                                                                                                                                                                                                                                                                                                            viral genome
                              TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                  LENGTH: 8202 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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   TELEPHONE:
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Best Local Simil
Matches 3966; (
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NAME/KEY:
US-08-258-420-13
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6 Becker Farm Road
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Patent No. 5710037
GENERAL INFORMATION:
APPLICANT: Vanin, Blio F.
TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR-NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271010-208
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,420
FILING DATE: 10-UIN-1994
CLASSIFICATION: 435
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ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette
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STATE: New Jers
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CCTTACTCTGTCATAACCTCTCAGACTAATGGTATGCGCATAGGAGACA 	5765 GCCTGAACTCCCATAAACCCTTATCTCTCACCTGGTTAATTACTGATCCGGCACAGGTA 5824  1884 ATGACAGCCCTCACCAGGTCTTCAATGTTACTTGGAGAGTTACCACTTAATGACAGGAC 1825  5825 TTAATATCAACAACACTCAAGGGGAGGCTCCTTTAAGAACCTGGTGGCCTGATGTAGG 5884		1764 TCGACTTGTGCGATTTAATAGGGGACGATTGGGATGAGACTGGACTTGGGTGTCGCATC 1705 5921 ÇÇCCAGATATCCTCÇATGCTCACGGATTTTATGTTTGCCCAGGACCACAAATAATG 5977		1644 CAACAGGGTGTGGAGGGCCGAGAGGGCTACTGTGGCAAATGGGGCTGTGAGACCACTG 1585 6038 ATGATGGATATTGGAAATGGCCAACCTCTCAGCAGGATAGGGTAAGTTTTCTTATGTCA 6097 1584 GACAGGCATACTGGAAGCCATCATCATCATGGGACCTAATTTCCTTAAGCGAGAA 1528	6098 ACACCTATACCAGCTCTGGACAATTTAATTACCTGACCTGGATTAGAACTGGAAGCCCCA 6157	6158 AGTGCTCTCCTTCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAAC 6214 .	6215 AAGAAAATATCCTAAAATGGTAAATGGTATGTTTGGGGAATGGTATATTATGGAGGCT 6274 1407 AGGCCAGCTGGGATGGCCCCAAAGTATGGGACTAAGACTGTACCAATCCA 1357	6275 CGGGTAAACAACCAGGCTCCATTCTAACTATTCGCCTCAAAATAAACCAGCTGGAGCCTC 6334	6335 CAATGGCTATAGGACCAAATACGGTCTTGACGGGTCAAAGACCCCCAA 6387 	6388GGACCAGGACCATCCTCTAACATAACTTCTGGATCAGACCCCACTG 6433	6434 AGTCTAACAGCACTAAAATGGGGCAAAACTTTTTACCTCATCCAGG 6484	6485 GAGCTTTTCAAGCTCTTAACTCCACACTCCAGAGGCTACCTCTTCTTGTTGGCTATGCT 6544	6545 TAGCTTCGGGCCCACCTTACTATGAAGGAATGGCTAGAAGGGGAAATTCAATGTGACAA 6604 16	6605 AAGAACATAGAGCACATGGGGATCCCAAAATAAGCTTACCCTTACTGAGGTTT 6664 	6665 CTGGAAAAGGCACCTGCATAGGAAAGGTTCCCCCATCCCACCACCCATTGTAACCACA 6724 	6725 CTGAAGCCTTTAATCAAACCTCTGAGAGTCAATATCTGGTACCTGGTTATGACAGGTGGT 6784
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PUBLICATION INFORMATION:
NUTIORS: JUKKA, J Wallchiewicz, J; Milosavljevic, A
AUTHORS: JUKKA, J Wallchiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
JOURNAL: JOURNAL: JOURNAL SEGURAL SEGURA SEG
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20.5%; Score 1663.6; DB 3; Length 7392;
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GAGACTTGCAGACCCACCCTTCCAGGGGGGACTCCGTCTAGACGCACCC 5523
GTGCAGGAAACCTCGAGCCCTTCCGGGGGGACTCCGTACTTTGACCACCAA 5583
GTGCAGGAAACCTCGAGAACGGCCCTTATCTCGTACTTTTGACCACACCAA 5583
GTTCTCAGGGAAACGGCCTTAATCTCGTACTTTTGACCACACCAA 5583

 Qy
 5584 GGCTGTGAAAGTCGAAGGAATCTCCACCTGGATCCAAGGTTAAACCGGCGC 56

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 5468 CAGCCATAAAGGTTGACGGAATCGCCACGTGGATTCACGCATCCCACGCAAGGCTGCTC 55

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rch completed: February 5, 2006, time: 1230 secs

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Run on:

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Searched:

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Sequence 3, Application US/10723552 V
Publication No. US20040185435A1
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: BOSCOL

CUTY: BOSCOL

STATE: MASSACHUSELTS

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/723,552

PRIOR APPLICATION NUMBER: US/9661,858
FILING DATE: CLNCHOWN:
APPLICATION NUMBER: US/9661,858
FILING DATE: CLNCHOWN:
APPLICATION NUMBER: US/9661,858
FILING DATE: CLNCHOWN:
ATTORNEY/ABOT INFORMATION:
TELECOMMUNICATION NUMBER: MGP-038CP
US-10-441-949-35
US-10-441-949-37
US-10-029-656-1
US-10-029-656-3
US-09-854-867-44
US-09-970-597-2
US-09-970-597-2
US-09-970-597-2
US-09-81-859A-25
US-09-10-113-664A-4
US-10-441-949-7
US-10-441-949-17
US-10-226-68-18
US-10-264-839-4
US-09-851-859A-24
US-09-851-859A-24
US-10-113-664A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TYPE: nucleic acid
STRANDEDNESS: single
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           Sequence 138, App Sequence 13, Appl Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 85, Appli Sequence 85, Appli Sequence 85, Appli Sequence 62, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Appl
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17580.806 Million cell updates/sec
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Sequence 139, App
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                       Sequence 33,
Sequence 39,
Sequence 41,
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1: /cgn2 6/ptodatal/lyubpna/USO7 PUBCOMB.seq:*
3: /cgn2 6/ptodatal/lyubpna/USO8 PUBCOMB.seq:*
3: /cgn2 6/ptodatal/lyubpna/USO8 PUBCOMB.seq:*
4: /cgn2 6/ptodatal/lyubpna/USO9B PUBCOMB.seq:*
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6: /cgn2 6/ptodatal/lyubpna/USO9B PUBCOMB.seq:*
7: /cgn2 6/ptodatal/lyubpna/USO9B PUBCOMB.seq:*
8: /cgn2 6/ptodatal/lyubpna/USO9C PUBCOMB.seq:*
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9: /cgn2 6/ptodatal/lyubpna/USO9C PUBCOMB.seq:*
10: /cgn2 6/ptodatal/lyubpna/USO9C PUBCOMB.seq:*
                                        GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-175-523-65

US-10-09-266-62

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US-10-09-266-16

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US-10-09-266-16

US-10-09-26-16

US-10-17-553-85

US-10-17-593-31

US-10-441-949-31

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US-10-677-558-5
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Result No.

Desire   Martch   100.01, Pred. No. 0, 10, Indate 1912;   Desire		1201 GCCAATTGCAGCCCCTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGGAAAA 1 1261 CTAACCATCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGGAGCATCCCTTA 1 1261 CTAACCATCCCCTTTCTCGGAGGATCCCCAACGCCTCACGGGGTTGGTGGAGCTCCCTTA 1 1261 CTAACCATCCCCTTTCTCGGAGGATCCCCCAACGCCTCACGGGGGTTGGTGGAGCTCCCTTA 1	1321 TGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCACAA 1 1321 TGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCACAA 1 1321 CCGAGGAGCAGAGAATTCTATTAGAGCTAGAAAAAATGTTCCTGGGGCCGACGGGC 1 1381 CCGAGGAGAGAAATTCTATTAGAGCTAGAAAAAATGTTCCTGGGGCCGACGGGC 1 1381 CCGAGGAGAAGAATTCTATTAGAGCTAGAAAAAAACTTCCTGGGGCCGACGGGC 1 1381 CCGAGGAGGAGAAATTCTATTAGAGCTAAAAAAAACTTCTTCGAGCCCGACGGGC 1	GACCCACGCGGTTGCAAATGAGATTGACATGTCCCTTAACTCGCCCCGGTTGGG 	ACTACAACAGGGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTCTGGTGGCGG	1561 GICTCCGGGGCGCCTCAAGACGGCCCACTAATTTGGCTAAGGTAGAGAAGTGATGCAGG 1 1621 GACCGAATGAACCCCCCTCTGTTTTTCTTGAGGGCTCTTGGAAGCCTTCAGGCGGTACA 1 1621 GACCGAATGAACCCCCCTCTGTTTTTCTTGAGAGGCTCTTGGAAGCCTTCAGGCGGTACA 1 1621 GACCGAATGAACCCCCCTCTGTTTTTCTTGAGAGGCTCTTGGAAGCCTTCAGGCGGTACA 1	CCCCTTTTGATCCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCTTTATAGGAC 	41 AGTCAGCCTTGGATATTAGAAAGCTTCAGAGACTGGAAGGGTTACAGGAGGCTGAGT		GGGGAACHAGGAGGGGGAAGAGGAAGGAAGGGAAGGGAA	AGAAGAATTTGACTAAGATCTTGGCTGCAGTGGATGGAAAGGAAAAGCAATACGGAAAAGAGAAAGAGAATTTGACTAAGAGTTGAAGGAAAAGGAATACGGAAAAGAGAAAGAGAAAGAGAAAGAGAAAAGAAAAGAAAA	1981 AGAGAGTTTTAGGAAAATTAGGTCAGGCCCTAGACAGTCAGGGAACCTGGGCAATAGGA 2 	2041 CCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAAAG	2101 GCCCCAAGAAGGAAACAAAGGACCAAGGATCCTAGCTCTAGAAGAAGATAAAGATTAGG 2
inilarity 100.0%; Score 8132; DB 8; Length 8132; Conservative 0; Manatches 0; Indels 0; Gaps of conservative 0; Manatches 0; Manatches 0; Indels 0; Gaps of conservative 0; Manatches 0; Man	8 8 8 8 8	9	8 8 8 8	oy Oy	8 8 8	8 8 8	oy Q	S B &	à 8 á	<u> </u>	B 5	9 8	රු අ	ò
	100.0%; Score 8132; DB 8; Length 8132; ; Conservative 10.0%; Pred. No. 0; ; Conservative 0; Mismatches 0; Indels 0; Gaps GCGTGGTGTACGACTGTGGGCCCCAGGGGCTTGGATAAAAATCCTCTTGCTGTTTGCA 60 GCGTGGTTACGACTGTGGGCCCCAGGGGCTTGGATAAAAATCCTCTTGCTGTTTGCA 60 GCGTGGTTACGACTGTGGGGCCTTGGATAAAAATCTCTTGCTGTTTTGCA 60 TCAAGACCGCTTCTCGTGAGTGATTAAGGGGAGTCGCTTTTCCGAGGCTTGTT 12	TTTGCTGGTCTTACATTTGGGGGTCGTCGGGATCTGTCGCGGCCACCCTAACAACCG 18	GTCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGCGCGCTTTCGGTTTGCAGCTGTCCTCTCTCT	AGGCCGTAAGGGCTGGGGAACTGTGATCAGCAGACGTGCTAGAAGGATCACAGGCTGCTG 3 CCCTGGGGGACGCCCGGGAAGGTGAAGAGCCAGGGACGCCTGGTGGTCTCCTACTGTC 4	GGTCAGAGGACCGAATTCTGTTGCTGAAGCGAAAGCTTCCCCCTCCGCGACCGTCCGACT	CTTTGCCTCCTTGTGGAAGACGTGGGGTCACGTGTGTCTGGATCTGTTGGTTTCTG TTTTGTGTGTCTTTGTCTTGTGTGTCCTTGTCTACAGTTTTAATATGGGACGGGGAA TTTTGTGTGTCTTTGTCTTGTGTGTCCTTGTCTTACACATTTTAATATGGGACACACGGTGA	CGACCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCCAGGGCTCATAATT	TGTCAGTTCAGGTTAAGAAGGACCTTGSCAGACTTTCTGTGTCTCTGAATGGCCGACAT	TCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAGATTATCCTGGCTGTTAAAG 	CAGITALITITCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCTATATCCTTACGT 84	GGCAAGATTTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATAAGCCAAGAA	AGCCAGGTCCCGGAATTCTGGCTCTTGGAGAAAACAAACA	AGCCCTCTCCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGGAACCCAAT	CTGTTCCCCCACCCCTTATCTGCCACAGGTGCCGCGAGGGGACCCTTTGCCCCTCTG

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APPLICANT: Diamond, Lisa E.
APPLICANT: Logan, John S.
APPLICANT: Logan, John S.
TITLE OF INVENTION: Retrovirus
FITLE OF INVENTION: Retrovirus
FITLE OF INVENTION: Retrovirus
FILE REPERRICE: 63066,00009
CURRENT APPLICATION NUMBER: US/10/113,664A
CURRENT FILING DATE: 2002-03-28
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 139
LENGTH: 8916
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ilarity 91.4%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Similarity
Matches 7574; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Sus scrofa
FEATURE:
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CAGGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGCTACCTCTTCTTGGCTA
                          TGCTTAGCTTCGGGCCCACCTTACTATGAAGGAATGGCTAGAAGAGGGAAATTCAATGTG
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; Sequence 1, Application US/10471220
; Dublication No. US20040142449A1
; GENERAL INPORMATION:
APPLICANT: Tonjes, Ralf R.
; APPLICANT: Tonjes, Ralf R.
; TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES
TITLE OF INVENTION: FROM FIG AND HUMAN CELLS
; TITLE OF INVENTION: FROM FIG AND HUMAN CELLS
; TITLE OF INVENTION: ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DEF;
; TITLE OF INVENTION: FOR PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DEF;
; TITLE OF INVENTION: ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DEF;
; FILE REFERENCE: 11692-007161
; CURRENT APPLICATION NUMBER: US/10/471,220
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: DE 101 11 433.8
; PRIOR APPLICATION NUMBER: DE 101 11 433.8
; PRIOR RELING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FASTSEQ for Windows Version 4.0
; TEMPORAL ON 10
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                           -----CTATTTGAGATAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: source
LOCATION: (0)...(0)
OTHER INFORMATION: Porcine cell line PKIS; replication-competent
OTHER INFORMATION: PERV-A clone PKIS-PERV-A(58)
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ORGANISM: Sus scrofa
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                                 GGAAATTCAATGTGACAAAAGAACATAGAGACCAATGCACATGGGGATCCCAAAATAAGC
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AGTTCTAAGATTAGAACTATTAACAAGAGAAGAAGGAGGAGAATGAAAGGATGAAATACA
                   AGTITGITCCITATAGGIAAAGATIAGGITITITTGCTGITITAAAAIATGC-----;
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                                                                  -----AAGCTAATGAGAAGCTTAAAATTGTTCTGAATTCCAG
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publication No. US20030224350A1

GENERAL INFORMATION:

APPLICANT: Cui, Cunqi

APPLICANT: Cui, Cunqi

APPLICANT: Logan, John S.

APPLICANT: Logan, John S.

TITLE OF INVENTION: Retrovirus

TITLE RETROVIRUS

TITLE OF INVENTION: Retrovirus

TITLE RETROVIRUS

TITLE RETROVIRUS

TITLE OF INVENTION: Retrovirus

TITLE RET
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ORGANIEM: Sus scrofa
FEATURE:
OTHER INFORMATION: porcine endogenous retrovirus (PERV)
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                                                                ACCT-----
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LENGTH: 8918
TYPE: DNA
ORGANISM: SUB SCIOÉA
FEATURE:
NOME(FEY: SOULE)(0)...(0)
OTHER INFORMATION: POICINE primary fibroblasts; replication-competent
OTHER INFORMATION: PERV-A clone PERV-A (Bac-130A12)
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                                                                                                   Query Match

84.0%; Score 6832.4;

Best Local Similarity 91.0%; Pred. No. 0;

Matches 7542; Conservative 1; Mismatches
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                                                                                      TYPE: DNA
CRGANISM: Sus scrofa
PEATURE:
OTHER INFORMATION: G3 locus; G3 PERV genome
US-10-113-664A-137
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                                                                                                                                                                             Query Match 78.0%; Score 6343.4; DB 6; Best Local Similarity 87.2%; Pred. No. 0; Matches 7175; Conservative 0; Mismatches 926;
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/279,337
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 139
SEQ ID NO 137
LENGTH: 8764
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Sequence 2, Application US/10471220
Publication No. US20040142449A1
Publication No. US20040142449A1
APPLICANT: Tronjes, Ralf R.
APPLICANT: Trach, Ulrich
TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES
TITLE OF INVENTION: REPLICATION ENDOCEDNOUS RETROVIRUS CLASS A AND CLASS
TITLE OF INVENTION: PROM PIG AND HUMAN CELLS
TITLE OF INVENTION: PROM PIG AND HUMAN CELLS
CURRENT APPLICATION NUMBER: US/10/471,220
CURRENT APPLICATION DATE: 2003-09-08
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PRIOR APPLICATION NUMBER: PCT/EP02/02656

PRIOR FILING DATE: 2002-03-11

PRIOR PELING DATE: 2001-03-09

PRIOR FILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

GRADINAR: PATGA

TYPE: DNA

ORGANISM: Sus scrofa

FEATURE:

NAME/KEY: SOURCE

LOCATION: (0)...(0)

OTHER INFORMATION: PERV-B clone PKI5: PERV-B(213)

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(8763)

OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                Score 6319; DB 7; Length 8
Pred. No. 0;
0; Mismatches 941; Indels
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Best Local Similarity 87.0%;
Matches 7159; Conservative
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## APPLICANT: Krach, Ulrich

TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES

TITLE OF INVENTION: OF PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DE

TITLE OF INVENTION: OF PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DE

TITLE OF INVENTION: FROM PIG AND HUMAN CELLS

FILE REFERENCE: 11692-007US1

CURRENT PAPLICATION NUMBER: US/04/71,220

CURRENT FILING DATE: 2003-09-08

PRIOR PLICATION NUMBER: DE 101 11 433.8

PRIOR PLING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 47

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 4

TENGRH: RALFORM MINDOWS VERSION 4.0

SEQ ID NO 4
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LOCATION: (0)...(0)
OTHER INDEMATION: Porcine primary fibroblasts; replication-competent
OTHER INFORMATION: PERV-B clone PERV-B(Bac-192B9)
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                                                                                                                                                                                          CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/10/723,552
FILING DATE: 26-Nov-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/661,858
FILING DATE: 14-Sep-2000
APPLICATION NUMBER: 08/766,528
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Pred. No. 0;
0; Mismatches
   IDIICATION NO. CUENTRAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE
AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
                                                                                                                  LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                 NUMBER OF SEQUENCES: 74
CORRESSONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8060 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  CITY: Boston
STATE: Massachusetts
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llarity 99.7%;
Conservative (
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                                                                                                                                                                                  COUNTRY: USA
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Best Local Similarity
Matches 5521; Conserv
   Publication No.
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                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REPERBOUS DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                       APPLICATION NUMBER: US/09/661,858
FILING DATE: 14-Sep-2000
APPLICATION NUMBER: 08/766,528
                                                                                           APPLICATION NUMBER: US/10/723,552 FILING DATE: 26-Nov-2003
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 7333 base pairs
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 79.4%;
Matches 6531; Conservative
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APPLICANT: Broans, David
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Rijancazk, Leszek
APPLICANT: Rijancazk, Leszek
APPLICANT: Rijancazk, Leszek
APPLICANT: Rajan, Prithi
APPLICANTON: WUMBER: US 60/299,151
PRIOR APPLICANTION NUMBER: US 60/299,151
PRIOR APPLICANTION NUMBER: US 60/317,828
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-25
PRIOR APPLICANTION NUMBER: US 60/325,150
PRIOR PLING DATE: 2001-09-11-14
PRIOR PLING DATE: 2002-01-11-14
PRIOR PLING DATE: 2002-01-18
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6335 GGBAACCTROCGCGCGATTGGGACCTGATGAGGATANACGAGGTATACTCGG 5134 637 GATTGGATTGGACCTCCGCCGCGATACCAGGACCTCTGGACATTTTACTCGG 5134 638 GATTGGATTGAGACCCCCCAGGAGGAAAAAACCCATCCGAAATTACCTGAAATTGGCTAGGATTGGTATTACCTTAAAATTACGCCCCCAGGAGGAAAAAAACCCATCCGAAAAATTACGCCCTACCTA
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Publication No. US20030096264A1
GENERAL INFORMATION:
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Best Local Similarity 60.1%;
Matches 4346; Conservative
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APPLICANT: BOACHMIN, OLLIEY
APPLICANT: BOACHMIN, OLLIEY
APPLICANT: Hock, Derek
APPLICANT: Klincak, Leszek
APPLICANT: Lessek
APPLICANT: Lessey
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Pithin
APPLICANT: 2002-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
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                                                                                                                                                                                                                                                  119897 TAGGTACAGGAACCGCTGCCTTAATTAAGACCCCCCCAATACTATGAAGAA-----
                                                                                                                                                                                                                                                                                                                   ACCTACATCGAATTGTAACAGAAGATCTCCAAGCCCTAGAAAAATCTGTCAGTAACCTGG
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                                                             AGAGAGAACCCATATCTCTGACACTTGCTGTGATGCTCGGACTTGGAGTGGCAGCTG
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114209 AAAAAATGTTCTGGGAGAGGACGGCACCCCCCCCCCCCTCCTCGTGGAGGC
                                                                                                                                                                                    114389 GGCTAAGGTAAGAGAGGTCTTGCAGGGGCAGACTGAACCACCCTCAGTCTTCCTTGAGCG
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                  ACAGCTGCTGCAGACCTCTTCACAACCGAGGAGCGAGAGAATTCTATAGAGGCTAG
                                                                                      AAAAAATGTTCCTGGGGCCGACGGGCGACCCACGCGGTTGCAAAATGAGATTGACATGGG
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                                                                                                                                                                           Score 2167.8; DB 10; Length 185548;
Pred. No. 0;
0; Mismatches 2582; Indels 299; Gaps
                                                                                                                                                                                                                                                     CCGTCCGACTCTTTTGCCTGCTTGTGGAAGACGTGGACGGGTCACGTGTGTCTGGATC-T
   60/361,834
PRIOR APPLICATION NUMBER: US 6(
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFFWARE: Patentin version 3.1
SEQ ID NO 62
                                                                                                                                                                             Query Match
Best Local Similarity 60.1%;
Matches 4346; Conservative
                                                                                      ; LENGTH: 185548
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-099-266-62
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4655 CAAAGAAGGATTAGAATATCTCCCTCCCATACTTTTTGAAGGGAAAATAGAATTGACTCC 117394  4655 CAAAGAAGGATTAGAATATGTCAACAGATACATCGTCTAACCCCTGAGGAACTAAACA 4714  117395 CGAAGAAGGAATAAAATTTGTGAAAGACTACCACCTGAGGAGTTGAAAA 117514  4715 CCTGCAGCAGTTGGTCAAAAATTCCCCTTATCATCTTCTGAGGCTACCAGGAGTGGCTGA 4774  117455 AATGATGAGTCAAAATTCCGATACCAAGTCCCCCAACTGCAAAGCTGGCTCA 117514  4775 CTCGGTGGTCAAACATTGTGTGCCCTGCCAGGTTAATGCTAATGCTAAAGCTACAAAGA 117574	4894 117634 4954 117694 5014	5074 117814 5134 117874 5194 117934		5428 118174 5488 118231	S489   CCAAGTGGGAGATTCAGGTTAGAGGCCACGGGGAAACTCGGAGATCGGGG   S548
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AIGCITAGCITCGGGCCCACCITACTATGAAGGAATGG 6577 TACTICAGAICATICT---CAATGICTTTGGGGAGAAA 119539 Agagaaidggtgtirraaaaacagcccccaggac 119011 AGGAAATAGGTGGGTTGGCGAGTATA---CCTTCCAC 119125 TCCACCAACTCCACACATAGTGGTACCCTCCC 119302 AAAGCCTACCTTGGCTTCCCCACCGCCCTAGGTACAG 119362 CCAGGGAGCTTTTTTAGCTTTAAATAGAACTAACCCTA 119422 |||| ||| || || Argagaaagcttactaaagccctcct 118891 Graecaaccacracaetccarcccraeacraer 118591 GCAGTTTTACCGAGCTAATCTTAGAGCTGCACAATTTT 118771 .ccccctacttataagitcaccgagaaagggaaacat19071 taacccicareciccaaricaacagictreggaagte 118531 crgraagiriagigecagarccaccaaargegaccrcc 118651 CCCACCCCTGAAGAGCGGTGTGTCCCAAACGGGATAG 118711 GAGCAAAAGGCTTCAACGAGAATGTGGAGGGGGATCAG 118831 -----TCCTCTAACATAACTTCTGGATCAGACCC 6428 ---GGTATTAATATCAACACTCCAAGGGGAGGCTCC 5855 ------GIGGCCIGAICTATACGTTTGCC 5890 GACCTCACCCCCAGATATCCTCCATGCTCACGGATTTT 5950 --CACCAAATAATGGAAAACATTGCGGAAATCCCAGAG 6001 CTGTGTAACCTCTAATGATGGATATTGGAA----- 6053 CTCAGCAGGATAGGGTAAGTTTTTCTTATGTCAACACC 6102 ATTACCTGACCTGGATTAGAACTGGAAGCCCCAAG--- 6159 TTACCTAAAATAAGTTTCACTGAGAAAGGAAAACAAG 6217 TGGTATGTCTTGGGGAATGGTATATTATGGAGGCTCGG 6277 AACTATTCGCCTCAAAATAAACCAGCTGGAGCCTCCAA 6337 CTTGACGGGTCAAAGACCCCCAACGACCAGGAC 6397 AAAA-----ATGG 6457 GACAAAAGAACATAGAGACCAATGCACATGGGGATCCC 6637 -GITCCITACICIGICAAIAACCICICAGACIAAIGGI 5748 ACTCCCATAAACCCTTATCTCTCACCTGGTTAATTACT

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LOCATION: (15939)...(16038)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (18223)...(18323)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (20974)...(21073)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (20974)...(21073)
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OTHER INPORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (2123)...[2222)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (3728)...[3827)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified base
LOCATION: (8849)...(8989)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
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PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 215980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTON: (24403)...(24502)
OTHER INFORMATION: a, t, c, g, ot
NAME/KEX: modified base
LOCATION: (27544)...(27673)
OTHER INFORMATION: a, t, c, g, ot
NAME/KEX: modified base
LOCATION: (30892)
OTHER INFORMATION: a, t, c, g, ot
NAME/KEY: modified base
LOCATION: (30801)...(31000)
OTHER INFORMATION: a, t, c, g, ot
NAME/KEY: modified base
LOCATION: (34443)...(34542)
OTHER INFORMATION: a, t, c, g, ot
NAME/KEY: modified base
LOCATION: (34443)...(34542)
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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                                                                                                                                                                                                                                                               NAME/KEY: modified_base
                                                                                                                                                                               TYPE: DNA ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119897 TAGGTACAGGAACCGCTGCCTTAATTAAGACCCCCCAATACTATGAAGAA------ 119946
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                                                                                                                                                                                                                                                                                                                                                      6818 CCACCTTGGTTTTTAACCAAACTAAAGATTTTTGCATTATGGTCCAAATTGTTCCCCGAG 6877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6938 AGAGAGACCCATATCTCTGACACTTGCTGTGATGCTCGGACTTGGAGTGGCAGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7058 ACCIACATCGAATTGTAACAGAAGATCTCCAAGCCCTAGAAAAATCTGTCAGTAACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGAATCCCTAACCTCCTTATCTGAAGTAGTCCTACAGAATAGAAGAGGGTTAGATTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6878 TGTATTACTATCCCGAAAAAGCAATCCTTGATGAATATGACTACAGAAATCATCGACAAA
           6638 AAAATAAGCTTACCCTTACTGAGGTTTCTGGAAAAGGCACCTGCATAGGAAAGGTTCCCC
                                                                                                                         6698 CATCCCACCAACACCTTTGTAACCACACTGAAGCCTTTAATCAAACCTCTGAGAGTCAAT
                                                                                                                                                                                                                                           6758 ATCTGGTACCTGGTTATGACAGGTGGTGGGCATGTAATACTGGATTAACCCCCTTGTGTTT
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Sequence 16, Application US/09972546
Sequence 16, Application No. US20030124704A1
GENERAL INFORMATION:
APPLICANT: STRITTWATTER, STEPHEN M.
APPLICANT: CATE, RICHARD L.
APPLICANT: SAH, DINAH W.Y.
TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
FILE REFERENCE: Alleges.
CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT PILING DATE: 2001-10-06
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ON: (42393) INFORMATION: EY: modified	ON: (42461) INFORMATION: EY: modified	INFORMATION: EY: modified	INFORMATION: EY: modified	See 3	INFORMATION: EX: modified	ON: (62818). INFORMATION: EY: modified	ON: (68518) INFORMATION: EY: modified	ON: (68534). INFORMATION: EV: modified	(74552) RMATIC	EY: modified ON: (81446). INFORMATION:	modified (88519).	INFORMATION: EY: modified	INFORMATION:	ON: (93794)	modified (96565)	MODIFIE	(96570 RMATIC	(96579)	INFORMATION: EY: modified ON: (96590)	INFORMATION: KEY: modified	INFORMATION: EY: modified	INFORMATION: EY: modified	~ -		ON: (96633) INFORMATION: EY: modified	
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168273 GCTGCCGTCAGGGAATTGTTTTCAGGAGGAA---GGGGGTCACCCTGATCAGATCCCC 168329 167977 égécéarcreárrictringagriécriérégacadácecadagredececedrireregrific 168036 528 CIGITGGITTCTGTTTTGTGTCTTTGTCTTGTGTCCTTGTCTACAGTTTTAATATG 168037 rirrirgiciragicicaigicaccicrigirgiciaciaciatri----icragaaato 768 CTGGCTGTTAAAGCAGTTATTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCC 469 GACCGTCCGACTCTTTGCCTGCTTGTGGAAGACGTGGACGGGTC-ACGTGTGTCTGGAT 588 GGACAGACGGTGACGCCCTCTTAGTTTGACTCTCGACCATTGGACTGAAGTTAAATCC 708 GAATGGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATTCTGAGATTATC Gaps DB 3; Length 215980; Score 2113.2; DB 3; Length 21598 Pred. No. 0; 0; Mismatches 2658; Indels 269; INCATION: (127063). (127162)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (131913). (139232)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (151051)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (153242). (153341)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (164706)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (164706)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (164706)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (164708)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
ILOCATION: (164708)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base NAME/KEY: modified base
LOCATION: (104447)...(104546)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (114521)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base LOCATION: (192192)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base
LOCATION: (198842)

OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base LOCATION: (182242) ... (182341)
OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified base or unknown other or unknown other or unknown or unknown LOCATION: (164710)...(164809)
OTHER INFORMATION: a, t, c, g, other
NAME/KEY: modified base LOCATION: (114527); (114626)
OTHER INFORMATION: a, t, c, g, other
NAME/KEY: modified\_base ο΄ σ ς, Ω Query Match
Best Local Similarity 59.4%;
Matches 4287; Conservative INFORMATION: a, t, CEY: modified\_base LOCATION: (192158) OTHER INFORMATION: a, t, NAME/KEY: modified base В 셤 g ઠે g ò δ g ò ò ò

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170466 3045 170526 3105 170586	3045 GC 3045 GC 170526 GC	3105 AT 170586 CT	3165 AC     170646 AC	3225 GA 170706 CA	3285 AZ     170766 AZ	3345 CC 170826 AC	3405 AZ	3465 GC 		3585 GC 		3705 AZ    171186 AZ	3765 A7	3825 CZ 	3884 GZ 			

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Mon Feb

	17	Oy 6366 GGGTCAAAGCCCCCAACCC Db 173963 TGTACCAGCTCCCCACCCC Oy 6411 AACTTCTGGATCAGACCCCC Db 174023 TCTCCTCATAAAGCCTACCT	Oy 6471 TAGCCTCATCCAGGAGCTTT 	174203	Oy 0551 CCITACIONS		DD 1/4410 IAAIAGIICCAAAAAIICC QY 6891 CGAAAAAGCAATCCTTGATC DD 174500 IAAIAGITCTTTTTTAGAII CV 6851 ATCTCTGACACTTGCTGTGA	174557 7011 174617		OY
5203 CTARATTGACCGCGGAGACTGCGTTAATGATTGGATAGCTCTCCTGCCCTTTGTGCTTT  172657 CTARATTAGCCATTGAGACCGGCAGAAAAGACTGGGTGGTGTCTCCTTCCT	5323 GACCCCCCATTGGTAGAAATTGCTTCTGTACATAGTGCTCTT 5376 172766 GACTCCCCCTTAATGGAAGCTGGTGGACTTTCCGACTCTGACCCTTTAC 172825 5377 CCCAGCCTTTGTTCTCTAGGCTCAAGGCACTTGGGTGGGT	5437 AACTCCGGGAGGCTACTCAGGAGGAGACTTGCAGATCCCACATGGTTTCCAAGTGG 5496		173063 TCCACG 5662 GGAAAG 173123 GGACAG	5708 173183 GACCTA 5757 AGGAGA	173243 AAGGAAACATTGTATGGGCAACCACTGCAGTCCATCCCCTCTGGATTTGGTGGCCTGAT 173302	173363 ACTGATCTTAGCAACCCACCCCTGAGGAGCGGTGTCCCAAATGGGATAGGAGAGCACA 173422 5899 GTTATTCCTAGTCTCACCCCCAGATATCCTCCATGCTCACGGATTTTATGTTTGC 5958 173423 TATGGGTGTTCGGGGCAGTTCTACCGAGCTAATCTTAGAGCTGCACATTTTTATGTTTGC 173482	5959 173483 6010	173543 TGTGGTAÀTGGACATGTGAÀCGACAGGAGÁTGCTTÁCTGGÀAGCCCTCTCTÀAATGG 173602  6067 CAGCAGGATAGGTAAGTTTTCTTATGTCAACACCTATACCAGCTCTGGACAATTAAT 6126  173603 GACCTAATCACGGTAAAACGAGTAGTGGCTATGATAAAGTCAAAGGAGAAAGAA	6127 TACCTGACCTGGATTAGAACTGGAAGCCC
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CCTACAGAATAGAAGAGTTAGATTTATTTTTTTAAAAGA 7190 cccccaatacratgaa------gaacracgracagr 174665 ACTATAGAACAGTCTATAACCAAATTAGAAGAATCTTTAAC 174725 Agadesectriereseceses accicas estadas de 174319 SAACATCCAGTCTAGCAAAAGCGGTCAGTATCTGGTGCCTCC 174379 ariaggidegringgegagraracariccacriaagagarder 173842 GATTGACAGTGAGAGCCCGGCAGTGACACTCGTAGGGCCC 173902 saddacccccagrcgracfgcrccccaaaggrccgac 173962 rraderriceceaececeeragaacadada controcereitad 174082 rtrtrtagrictaaaragaactaacccraarargacrcaarc 174142 6365 6530 rrcegecccaccrracrargaaggaarggcragaagaggaa 6590 ACATAGAGACCAATGCACATGGGGATCCCAAAATAAGCTTAC 6650 AAAAGGCACCTGCATAGGAAAGGTTCCCCCCATCCCACCAACA 6710 AGCCTTTAATCAAACCTCTGAGAGTCAATATCTGGTACCTGG 6770 ATGTAATACTGGATTAACCCCTTGTGTTTCCACCTTGGTTTT 6830 rrecarrargerccaaarrerreceeaagrerarracrarec 6890 IGAATATGACTACAGAAATCATCGACAAAAGAGAGAACCCAT 6950 7130 CTTGAAGGAGGAATGCTGTTTTTATGTGGATCATTCAGGGGC 7250 6313 PACTGAGICTAACAGCACGACTAAATGGGGGCAAAACTTTT 6470 SGTAAATGGTATGTCTTGGGGAATGGTATATTATGGAGGCTC 6275 ITITICAAGCICITAACTCCAGACTCCAGAGGCTACCTCTTC TTGCAATACCGGTCTCACTCCTTGTGTGTCTATGTCTGTTTT -----CATTCTAACTATTCGCCTCA SCTGGAGCCTCCAATGGCTATAGGACCAAATACGGTCTTGAC CAA-----CGACCAGGACCATCCTCAACAT ACCACAGCAGCTAGAACAGGACTTAGTAACCTACATCGAAT AGCCCTAGAAAATCTGTCAGTAACCTGGAGGAATCCCTAAAC

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7371 TTCTGCTTTAACAGGACCCTTAATAGTCCTCCTCTGTTACTCACAGTTGGGCCATGTAT 7430
                                     174846 AATCAAAGATTCTATGGCTAAACTTAGAGAAGGCCTAGATATAGGTAAAGAGAAAAAA 174905
                  7251 CATCAGAGACTCCATGAACAGCTTAGAGAAAGCTTGGAGAGAGCGTCGAAGGGAAAAGGA 7310
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Job time : 4181 secs
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Sequence 7, Appli
Sequence 6, Appli
Sequence 1069, Ap
Sequence 1069, Ap
Sequence 79, Appl
Sequence 79, Appl
Sequence 1324, A
Sequence 1324, A
Sequence 1324, A
Sequence 1327, A
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 24, Appl
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1 GCGTGGTGTACGACTGTGGG.......CTGTTTGCATCAAAAAAA 8132
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1. /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

2. /cgn2_6/ptodatea/2/pubpna/US08_NEW_PUB.seq:*

3. /cgn2_6/ptodatea/2/pubpna/NS07_NEW_PUB.seq:*

4: /cgn2_6/ptodatea/2/pubpna/NS07_NEW_PUB.seq:*

5: /cgn2_6/ptodatea/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodatea/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodatea/2/pubpna/US10_NEW_PUB.seq:*

8: /cgn2_6/ptodatea/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodatea/2/pubpna/US11_NEW_PUB.seq:*

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GenCore version 5.1.7
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Sequence 77, Appl Sequence 13215, A	Sequence 13203, A	Sequence 1747, Ap	Sequence 5389, Ap	Sequence 1747, Ap	Sequence 5389, Ap	Sequence 13340, A	Sequence 13265, A	Sequence 9, Appli	Sequence 10, Appl	Sequence 16, Appl	Sequence 1, Appli	Sequence 2, Appli	Seguence 64, Appl	Sequence 63, Appl	Seguence 15, Appl	Sequence 17, Appl	Seguence 39, Appl	Sequence 40, Appl	Sequence 31, Appl	Seguence 50, Appl	Sequence 92, Appl
US-11-121-086-77 US-10-995-561-13215	US-10-995-561-13203	US-11-128-061-1747	US-11-128-061-5389	US-11-128-049-1747	US-11-128-049-5389	US-10-995-561-13340	US-10-995-561-13265	US-11-121-086-9	US-11-121-086-10	US-11-121-086-16	US-11-157-389-1	US-11-157-389-2	US-11-121-086-64	US-11-121-086-63	US-11-121-086-15	US-11-121-086-17	US-11-121-086-39	US-11-121-086-40	US-10-996-217A-31	US-11-121-086-50	US-11-121-086-92
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## ALIGNMENTS

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Sequence 8, Application US/10996217A
Sequence 8, Application US/10996217A
Publication No. US20050266561A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: Revivionor, Inc.
APPLICAMT: Wells, Kevin
TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
FILE REFERENCE: 10785.105070 REV 1015 US
CURRENT APPLICATION NUMBER: 60/523,938
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR APPLICATION NUMBER: 2003-11-21
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
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SEQ ID NO 8
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llarity 85.1%; Pred. No. 0;
Conservative 0; Mismatches 175; Indels 119;
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ORGANISM: Artificial Sequence
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in the Production of Transgenic Animals
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                                                                                 CAAAGAAGCTCGATCCTGTAGCCAGTGGTTGGCCATATGCCTGAAGGCTATCGCAGCTG 3759
                                                                                                                                                                                             TGGCCATACTGGTCAAGGACGCTGACAATTGACTTTGGGACAGAATATAACTGTAATAG 3819
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GGGCTCCTGAGCACCAGAAGGCATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACCTG
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Pred. No. 0;
0; Mismatches 186; Indels
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; Sequence 9, Application No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivitor, Inc.;
APPLICANT: Wells, Kevin
; TITLE OF INVENTION: Use of Interfering RNA in TITLE OF INVENTION: Use of Interfering RNA in CURRENT FILING DATE: 2004-11-22
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; RROM FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; TEALLY OF 95
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Best Local Similarity, 98.2%;
Matches 1471; Conservative (
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                                                         TAAAGCCTGATCAAATATACAATTCTGGTTGGAACAGTTTCCCCAAGCCTGGGCAGAA
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121   CCAAGATGGGAGCTCAATTCTTTGAACAAGGAAGACCAGAAGTGTCTGTGAATAACA 180	2920 TGTGTGCTCTCCGCCCCAACGGAGCTGGTATACAGTATTGGACTTAAAAGGATGCCTTCT 2979 601 TGAGCGCCTCCCGCCTGAACGGAACTGGTACAGTATTGGACTTAAAAGGATGCCTTCT 660 2980 TCTGCCTGAGATTACACCCCACTGGCAACGGTTTTTGCCTTCGAATGGAGAGATCCAG 3039 661 TCTGCCTGAGATTACACCCCACTGGCAACGGCTTTTGCCTTCGAATGGAGAGATCCAG 720 3040 GTACGGGAAGACCCGACTGCACCGCTTTTTTTTTTTTTT	3340 GGCAGCGATGGCTGACGGAGGCACGGAAGAAAATCTGTAGTCCAGATACCGGCCCCAACCA 3399 1010 GGCAGTGATGGCTGACGGAAGGAACTGTAGTCCAGATACCGGCCCCAACCA 3399 1010 GGCAGTGATGGCTGACGGAAGGAACTGTAGTCCAGATACCTTTTTTTT

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	RESULT 5 US-11-128-061-1069 is Sequence 1069, Application US/11128061 ; Publication No. US20060003958A1 ; GENERAL INFORMATION: ; APPLICANT: Melville, Mark W. ; APPLICANT: Mounts, William W. ; APPLICANT: Hann, Louane E. ; APPLICANT: Sinacore, Martin S. ; APPLICANT: Brown, Eugene L. ; APPLICANT: Louane E. ; APPLICANT: Sinacore, Martin S. ; APPLICANT: Louane E. ; APPLICANT: Louane E. ; APPLICANT: Louane E. ; APPLICANT: Christopher P.	TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS ; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION ; FITER REFERENCE: 0.1997.027701 ; CURRENT APPLICATION NUMBER: US/11/128,061 ; CURRENT APPLICATION NUMBER: US 60/570,425 ; PRIOR APPLICATION NUMBER: US 60/570,425 ; PRIOR FILING DATE: 2004-05-11 ; PRIOR FILING DATE: 2004-05-11 ; NUMBER OF SEQ ID NOS: 7285 ; SOFTWARE: Pacentin version 3.3 ; SEQ ID NO 1069 ; LENGTH: 9603 ; TYPE: DNA ; ORGANISM: Cricetulus griseus	FRATURE:  NAME/KEY: misc_feature  LOCATION: (598)(2723)  COTHER INFORMATION: n is a, c, g, or t  FEATURE:  NAME/KEY: misc_feature  LOCATION: (3361)(3353)  COTHER INFORMATION: n is a, c, g, or t  FRATURE:  NAME/KEY: misc_feature  LOCATION: (3791)(3889)  COTHER INFORMATION: n is a, c, g, or t  FRATURE:  FRATURE:  FEATURE:  FEATURE	NAME/KET: MIEC FEATURE  LOCATION: (4564). (4612)  PEATURE: NAME/KEY: misc feature  LOCATION: (4665). (4698)  OTHER INFORMATION: n is a, c, g, or t  FEATURE: NAME/KEY: misc feature  LOCATION: (5185). (5217)  OTHER INFORMATION: n is a, c, g, or t  FEATURE: NAME/KEY: misc feature  LOCATION: (5246). (5293)  OTHER INFORMATION: n is a, c, g, or t  FEATURE: NAME/KEY: misc feature  LOCATION: (5246). (5293)  OTHER INFORMATION: n is a, c, g, or t  FEATURE: NAME/KEY: misc feature  LOCATION: (5246). (5293)  CTEATURE: NAME/KEY: misc feature  LOCATION: (5314). (5351)
### ##################################	1068   TTTGCCCCTCCTGGAGCTCCGGCGGTGCAGCGACCTGCTGCAGGACTCGGAGCCCGAGG   1127	THIRD TO SHARE THE CONTROL OF THE CO	839   ĠĠĠĊĊĠĠĠĠĠĠĊĠĠĊĠĠĊĠĠĊĠĠĠŢŢĠĊĀĀĀŢĠĀĀŢŢĠŖĠŢŢĠĠĀŢŢĠĊŢŢĠĠŢŢŢĠĊĀĀĀŢĠŖĠŢŢĠĠĀĀŢŢĠĠĀĀŢŢĠĠĀĀŢŢĠĠĀĀĀŢŢĠĠĀĀĀŢŢĠŖĠŢŢĠĠĠĠĠĠĠĠ	

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AGAGCTCAAATACACTTTGAGAGGTCAGAAGTCAAAGTCACAGGGCCAGAGGGAATTCCC 3261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 835.6; DB 8; Length 9 44.2%; Pred. No. 6.2e-234; tive 0; Mismatches 2024; Indels
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i LCCATION: (9236)..(9277)
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LOCATION: (8919)..(8944)
OTHER INFORMATION: n is a,
                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (8803)..(8825)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.2<sup>†</sup>
Matches 1632; Conservative
                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (7935)..(8343)
OTHER INFORMATION: n is a,
                                   NAME/KEY: misc feature
LOCATION: (7322)..(7444)
OTHER INFORMATION: n is
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                                                                                        APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Sinacore, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
APPLICANT: MILLER CHRESSION AND METHODS FOR TITLE OF INVENTION: MAKING AND USING SAME FILER REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR PILING DATE: 2004-05-11
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                                     Sequence 1069, Application US/11128049
Publication No. US20060010513A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 1069
LENGTH: 9603
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NAME/KEY: misc_feature
LOCATION: (5185)..(5217)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (5699)..(6078)
OTHER INFORMATION: n is a,
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LOCATION: (3791)..(3889)
OTHER INFORMATION: n is a,
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LOCATION: (4504)..(4612)
OTHER INFORMATION: n is a,
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LOCATION: (4665)..(4698)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (3301)..(3353)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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INFORMATION: n is a,
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LOCATION: (5618)..(5648)
OTHER INFORMATION: n is a,
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LOCATION: (7036)..(7101)
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LOCATION: (5246)..(529
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LOCATION: (6145)..(629)
RESULT 6
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οp	3441 ATCCTTCCTGCATCCGTCAGACAGTATCCAATGCCTAAAGAAGCCCCGAGAAGGAATTCGG 3500
ò	2798
đ	3501 CCACATATTAAAAG-TTACTTGAACAAGGGATTCTGGTGCCCTGTAAATCTCCTTGGAAT 3559 Qy
ò	2799 ACTCCCTGCTACCGGTAGAAAGCCTGGGACTAATGACTATCGACCAGTACAGGACTTG 2858
ф	3619
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ò	TIGIGIGCTCTCCCAACCCAACGGAGCTGGTATACAGTATTGGACTTAAAGGATGCCTTC 2978
අූ	CTGAGCGGATTGCCACCCAACTATACCTGGTATACAGTCTTAGATCTTAAAGATGCCTTC
ò	2979 TTCTGCCTGAGATTACACCCCCTAGCCAACCACTTTTTGCCTTCGAATGGAGAGTCCA 3038
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qq	3800 INNINNINNINNINNINNINNINNINNINNINNINNINN
ò	3158
д	3860 NANNANANANANANANANANANANANANANANANANAN
ò	3159 CAGGTGACCCTCCAGTACGTGGATGACCTGCTTCTGGCGGAGCCACCAACAACAGGAC 3218
QQ	3920 GCGCTAATCCTCTTACAGTATGTAGATGACATCCTCCTGGCAGCCAAAACCAAGGAAGAA 3979
ò	3219 IGCTIAGAAGGCACGAAGGCACTACTGCAAATTGTCTGACCTAGGCTACAGAGCCTCT 3278
qq	3980 recaagaaadacacrecaagacccrecaagacrecragaagaccaagacaragaagaagacaragaagaagaagaagaagaagaagaagaagaagaagaag
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q	4100 ĠĠaĊĠĠĊĠĀTĠĠĊŢŖĀĊĠĠĀĀĠĊĊĠŢĀTĠĊĠĀĠĊĊĀŤĊŦŦĀĠĀĀŢŦĊĊĊĀĊĠĀĀ 4159 Qy
È	3399 ACAGCCAAACAATGAGAGTTTTTGGGGACAGCTGGTTTTGCAGACTGTGGATCCCG 3458
QQ	4160 Anteceeccaneridadadarretroganacadenderrerogeceecenarganeece 4219
ò	3459 GGGTTTGGGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAAAGGGGAATTCTCC 3518
QQ	4220 dedrirecceanaredecederecereratececerereseceneses 4279
ò	
q	4280 TGGGAAGAGCCCCAAAAGAAAGCCTTCACCAACATCAAAAAGGCTCTCCTTGAATCACCA 4339 QY
ò	
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ò	3639 GTAGCCCGGGGACTTTTAACCCCTAGGACCTTGGAGAAGACCTGTCGCCTACCTG 3698
g	
ò	3699 TCAAAGAAGCTCGATCCTGTAGGCAGTGGTTGGCCTATGCCTGAAGGCTATCGCAGCT 3758
đđ	4460 TCCAAGAAATTGGATCCTGTAGCATCGGGATGGCCACCCTGTCT-NNNNNNNNNNNNNNNNN 4518 Qy
ò	
qa	4519 NYKHNINKINKINKINKINKINKINKINKINKINKINKINKINK

3819 GC 4579 NR	GCCCCCCATGCATTGGAGAACATCGTTCGGCAGCCCCAGACCGATGGATG
3879 CC 	CGCATGACCCACTATCAAAGCCTGCTTCTCACAGAGAGGGTCACGTTCGCTCCACCAGCC 3938 
3939 GC   	GCTCTCAACCCTGCCACTTTCTGCCTGAAGAGCTGATGAACCAGTGACTCATGATTGC 3998 
3999 C? 4759 T?	CATCAACTATTGATTGAGAGACTGGGGTCCGCAAGGACCTTACAGACATACGCTGACT 4058
4059 GC 4819 AC	GGAGAAGTGCTAACCTGGTTCACTGACGAAGCTATGTGGTGGAAGGTAAGAGGTG 4118 
4119 GC 	getroggegegegegegegegegegegegegegegegegegeg
4179 AC   4939 AC	ACTICAGCACAAAAGGCIGAGCICAIGGCCCICACGCAAGCITIGCGGCIGGCCGAAGGG 4238 
4239 AJ   	aartccataaacatttataggacagcaggtatgcctttgcgactgcacacgtacatggg 4298 
4299 G(   5059 G	GCCATCTATAAACAAAGGGGGTTGCTTACCTCAGCAGGGAAAAAAAA
4359 GJ 1 5119 GJ	GAAATTCTAAGCCTATTAGAAGCCGTACATTTACCAAAAAGGCTAGCTA
4419 C   5179 C	CCTGGACATCAGAAAGCTAAAGATCTCATATCCAGAGGAAACCAGATGGCTGACCGGGTT 4478 
4479 G   5239 G	GCCAAGCAGGCAGCCCAGGGTGTTAACCTTCTGCCTATAATAGAAATGCCCAAAGCCCCA 4538 
4539 G 	GAACCCAGACGACGGTACACCCTAGAAGACTGGCAAGAGATAAAAAAAGATAGACCAGTTC 4598 
4599 T	TCTGAGACTCCGGAAGGGACCTGCTATACCTCAGATGGGAAGGAAATCTGCCCCACA 4656 
4657 A 5419 G	aagaagggttagaatatgtccaacagatacatcgtctaacccacctaggaactaaacacc 4716 
4717 T       5479 T	TGCAGCAGTTGGTCAGAACATCCCCTTATCATGTTCTGAGGCTACCAGGAGTGGC 4771 
4772 T       5539 T	tgactc-ggtggtcaaagattgtgtgcctgccagctggttaatgctaatccttccagaa 4830 
4831 T       5599 T	TGCCTCCAGGGAAGAGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCA 4890 

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-79
LENGTH: 177175
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                                         1951 CAGGATGGGTAGAGGCTTATCCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAAAAA 5010
                                                                                                      5131 IGCATTGIGCATACAGACCCCAAAGCTCAGGACAGGTAGAGGATGAATAGAACCATTA 5190
                                                                                                                                                                                         5251 CCTTTGTGCTTTTTAGGGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCCTATGAAT 5310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCCACCTGGATCCATGCATCCCACGTTAAACCGGCGCCCACCTCCCGATTCGGGGTGGA 5664
 CTGAGGTAAAGCCGGCTAAATACGGAAACAAATACCTATTGGTTTTTGTAGACACCTTTT 4950
                                                                                 5011 TACTGGAAGAATTTTTCCAAGATTTGGAATACCTAAGGTAATAGGGTCAGACAATGGTC 5070
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 79, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
    APPLICAMT: POULSEN, TIM S.
; APPLICAMT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT PILING DATE: 2005-05-04
; PRIOR PLING DATE: 2005-05-04
; RIOR APPLICATION NUMBER: 60/567,570
; RIOR APPLICATION NUMBER: 60/567,570
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin Version 3.3
; SEQ ID NO 79
                                                                                                                                                                                                                                    CGTGCTGCTTTCCCCAGCCTTTGTTCTCTAAGGCTCAAGGCACTTGAGTGGGTGAGACAACG
                                                                                                                                                                                                                                                                                                                                                              AGCGTGGAGGCAACTCCGGGAGGCCTACTCAGGAGGAGGAGCATGCAGATCCCACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5191 AAGAGACCCTTACTAAATTGACCGCGGAGACTGGCGTTAATGATTGGATAGCTCTCCTGC
                                                             5311 TACTCTACGGGGGACCCCCCCATTGCTAGAAATTGCTTCTGTACATAGTGCTGA----
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142831 AGAAACTCAGAAAGCCAATACCCATTTAGTAAGATGGACACTGAAGCAGAAGCAGACTTT 142890
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                                                                                                 2600 TCCCCAAGCCTGGCCAGAAACCGCAGGGATGGGTTTGGCAAAGCAAGTTCCCCCACAAGT
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                                                                                                                                              141949 TCCTGAAGTCTAAGCAACAGAAGGACAATATAGACGAGCAAAGAATGCCCATCCTGTTCA
                                                                                                                                                                                               AGCTCAAGAAGGAATTCGGCCGCATGTCCAAAGATTAATCCAACAGGGCATCCTAGTTCC
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                                                    Gaps
                                                 37;
Length 177175;
                                                 0; Mismatches 930; Indels
  Score 287; DB 8;
Pred. No. 1.1e-71;
  Query Match 3.5%;
Best Local Similarity 49.1%;
                                  Best Local Similarity 49.1
Matches 932; Conservative
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143427 TGGAAGTTCCTTTGTAGAAAAAGGACTTCAAAAAGTGGGGTATGCAGTGGTCAGTGATAA
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                                                              ACCCTTTACCCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGGAGTTTTAACCCAAAC
                                                                                                                                                         GATTGGCTTCATTGTTTACAGGTAGTGGCAGTAGCAGTAGCAGTCTTAGTGTCTGAAGTGGT
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APPLICANT: POULSEN, TIM S. APPLICANT: NIELSEN, KIRSTEN V. TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

Sequence 78, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:

RESULT 8 US-11-121-086-78

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                                                                                                                                                                                                                                                                                                            Length 189993;
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                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 930;
                                                                                                                                                                                                                                                                                                            Score 287; DB 8;
Pred. No. 1.2e-71;
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VECSION 3.3
                                                                                                                                                                                                                                                                                                       3.5%;
                                                                                                                                                                                                                                                                                                              3.5
Query Match
Best Local Similarity 49.1
Matches 932; Conservative
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Dain, Bradley
APPLICANT: Dain, Bradley
APPLICANT: Daton, R. Rex
APPLICANT: Denton, R. Rex
APPLICANT: Occemir, Vural
APPLICANT: Occemir, Vural
APPLICANT: Reed, Carol R
TITLE OF INVENTION: EPHX Genetic Markers Associated with Gala
FILE REFERENCE: 2300.0030001
CURRENT APPLICATION NUMBER: US/10/972,766
CURRENT FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/515,378
PRIOR APPLICATION UNMBER: 60/515,378
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Pred. No. 6.1e-66;
0; Mismatches 1218;
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OTHER INFORMATION: n is the reference allele
OTHER INFORMATION: allele 't'
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LOCATION: (26434). (26434)
THER INFORMATION: n is the reference allele
OTHER INFORMATION: allele 'c'
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                                             Sequence 1, Application US/10972766 Publication No. US20050250118A1 GENERAL INFORMATION:
                                                                                                                                   APPLICANT: Aerssens, Jeroen
APPLICANT: Athanasiou, Maria
APPLICANT: Cohen, Carlos
APPLICANT: Cohen, Nadine
APPLICANT: Dain, Bradley
APPLICANT: Deaton, R. Rex
APPLICANT: Deaton, R. Rex
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LOCATION: (26376).(26376)
OTHER INFORMATION: n is the re
OTHER INFORMATION: allele 'a'
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NAME/KEY: misc_feature
LOCATION: (54475).. (54475)
OTHER INFORMATION: n is the ru
COTHER INFORMATION: allele 'c'
US-10-972-766-1
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NAMB/KEY: misc_feature
LOCATION: (21845). (21845)
OTHER INFORMATION: n is the r'
OTHER INFORMATION: allele 'g'
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SOFTWARE: PatentIn version 3.3
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Best Local Similarity 49.2%;
Matches 1279; Conservative
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LOCATION: (46768) ..(46768)
OTHER INFORMATION: n is the 1
OTHER INFORMATION: allele 't'
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ORGANISM: Homo sapiens
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LOCATION: (11006)..(11
                            US-10-972-766-1/c
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                                                                                                                                                                12204 AGAAACTCAGAAAGCCAATACCCATTTAGTAAGATGGACACCTGAAGCAGAAGCAGCTTT 12263
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                                                12144 CTACCGAATGTGGATTCCCAGGTACAGCAAATAGGCAGATCATTATATACACTAATTAA 12203
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                                                                                                            --ATTCTCCTGGGCTCCTGAGCACCAGAAGGCATT
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\$816 CROCAGCOCCCCAGACCGATCACACCCCCCCACTACCCCCCCTTACACTCCTCTCTTS \$818 GTTCCCAAACCACTCCTCCCCCCCCCCCCCCCCTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCCCCCC
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1810 GICCANTCTCCTGGANTAGTCCCTGCTAGGANTAGANGCCTGGGACTANTCTCGGGANTATTCGGCGANGCCTAGGGGG 6336 2811 GICCANTCTCCTGGANTGGAGGAGTCAGANGCCTGGGATATTCCTCGGCANGCCT 2010 6513 GGACTGGAGGAGTCGGAGGAGTCAGAGGAGTAGTCCTGGCGAGTATTCCTCGCACAGCTC 2010 6513 GGACTGGAGGAGTCGGAGGAGAGTCAGGAGAGTCAGTTGGCGAGTATTCCTCTGCGCAGAGTCTTTGGCGAGTATTCCTCTGCAGAGTCAGTTTTTGGCGAGTAGTCGCAGAGTCAGTTTTTGGCGAGTAGTCGCAGAGTCAGTTTTTGGC 6416 6513 GGCTCAGGAGTCCTCTCTCTCTCTCTCCTCAGAGTCAGAGTCTTTTTGGC 6416 1011 ITTCAGAGTCAGTCTTCTCTCTCTCTCAGATCTCTTCTCT

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TICACCIGGACIGACCCTGACACCCTCCAGICACAACAACACACATGACTGICCTCCCT 2288
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Tache-Crain, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preering Reference: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOCTHARE: PL_SEQ_genes Version 1.0
SEQ ID NO 357
LENGTH: 5234
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3.1%; Score 253.6; DB 7;
Best Local Similarity 47.8%; Pred. No. 5.1e-63;
Matches 1232; Conservative 0; Mismatches 1269;
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Publication No. US20050255114A1
GENERAL INFORMATION:
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US-10-821-234-357
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US-10-821-234-357
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                                                                                                                                                                                                                                                                                                                                                                                  G, or insertion/deletion polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Length 110711;
                                                                                   APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, ITLLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
SURENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PASSES OF OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%; Score 218.4; DB 7; Length Best Local Similarity 49.3%; Pred. No. 1.2e-51; Matches 914; Conservative 5; Mismatches 891; Indels
                              ; sequence 13264, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

// LOCATION: (1)...(110711)

// OTHER INFORMATION: n = A,T,C or

US-10-995-561-13264
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
RESULT 11
US-10-995-561-13264/c
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                                                                                                          ATAGCTCTCACCAGGCCCTAAATCTTTCCAAAGGCAAACGAGTCAACATTTATACAGAC
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Pred. No. 1.5e-47;
0; Mismatches 220; Indels
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APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION Probe Arrays For Expression Profiling
FILE REFERENCE: 031896-041000 (AN101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
FRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PALENTIN Version 3.2
                                                                                                                                                       ; Sequence 3585, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.8%;
Matches 376; Conservative
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US-11-136-527-3585/c
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT PAPLICATION UNMERS: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 13227
LENGTH: 317876
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Pred. No. 5.1e-46;
5; Mismatches 876;
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S-10-995-561-13227
Sequence 13227, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local Similarity 48.5%;
Matches 918; Conservative
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                                                                                                                                                                                                                                                         2.0%; Score 162.6; DB 7;
94.9%; Pred. No. 2.3e-37;
tive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 5, 2006, 07:04:51 Job time: 1217 secs
                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Construct US-10-996-217A-24
                          SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 180
                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.91
Matches 168; Conservative
     NUMBER OF SEQ ID NOS: 272
                                                                                                                                                          FEATURE:
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US-10-996-217A-20/C

US-10-996-217A-20/C

Squence 20, Application US/10996217A

Publication No. US20050266561A1

GENERAL INFORMATION:

APPLICANT: Revivior.

TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals

FILE REPRENCE: 10785.105070 REV 1015 US

FILE REPRENCE: 2004-11-22

PRIOR APPLICATION NUMBER: 05/10/996,217A

CURRENT FILING DATE: 2004-11-22

PRIOR APPLICATION NUMBER: 60/523,938

PRIOR PILING DATE: 2003-11-21

NUMBER OF SEQ ID NOS: 272

NUMBER OF SEQ ID NOS: 272

SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
FILE REFERENCE: 10795.10570 REV 1015 US
CURRENT APPLICATION NUMBER: US/10/996,217A
CURRENT FILING DATE: 2004-11-22
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR FILING DATE: 2003-11-21
122184 CTAACCTCTGGGGGAWCCCCTATTAAATACCACAAGGAAATCATGGAGTTATTGCACTCA 122243
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Best Local Similarity 93.6%; Pred. No. 4.3e-43;
Matches 190; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                      4443 CTCATATCCAGAGGAAACCAGATGGCTGACCGGG 4476
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Publication No. US20050266561A1
GENERAL INFORMATION:
APPLICANT: Revivicor, Inc.
APPLICANT: Wells, Kevin
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US-10-996-217A-24/c
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